

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 24, 2006, 01:16:00 ; Search time 194 Seconds
(without alignments)
1121.830 Million cell updates/sec

Title: US-10-679-362-2

Perfect score: 2469

Sequence: 1 MSTQRLRNEDYHYSSTDVS.....YELIQSNAPFINSTCAPI 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*
- 10: geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2469	100.0	476	7	Adf90164 Human tra
2	2469	100.0	476	8	Adr03799 Human nov
3	2466	99.9	507	6	Abg75834 Transport
4	2461	99.7	476	6	Abp96441 Human tra
5	2460	99.6	496	6	Abu52588 Human NOV
6	2402.5	97.3	568	5	Aaol14191 Human tra
7	2398	97.1	500	6	Abu52587 Human NOV
8	2324	94.1	476	4	Abu52587 Human NOV
9	2324	94.1	476	7	Adf90169 Human tra
10	2324	94.1	476	8	Adr03804 Human hom
11	2217	89.8	434	6	Ada55508 Human pro
12	2217	89.8	434	8	Adsl11015 Human the
13	2146.5	86.9	475	6	Abp96446 Rat LYAAT
14	2144.5	86.9	475	6	Abp96443 Mouse tra
15	2142.5	86.8	475	4	Abb76935 Rat VG51.
16	1723	69.8	382	4	Abb76934 Rat VG41.
17	1722.5	69.8	483	5	Abp98199 Human HIP
18	1722.5	69.8	483	6	Abp96437 Human tra
19	1718.5	69.6	483	5	Aae26625 Human tra
20	1718.5	69.6	507	8	Adn33124 Human tra
21	1718.5	69.6	507	6	Aae29907 Human tra
22	1713.5	69.4	483	8	Adg65947 Novel hum
23	1696.5	68.7	478	6	Abp96435 Mouse tra

24	1677.5	67.9	481	6	ABP96436	Abp96436 Rat trand
25	1544	62.5	450	5	ABB98200	Abb98200 Human HIP
26	1539	62.3	450	8	ADJ27216	Adj27216 Human TRI
27	1476.5	59.8	470	6	ABP96438	Abp96438 Human tra
28	1476.5	59.8	470	6	ADR09715	Adr09715 Human pro
29	1463	59.3	433	8	ADP28500	Adp28500 Human sec
30	1461	59.2	431	8	ADP29656	Adp29656 Human sec
31	1448.5	58.7	427	5	AAE25571	Aae25571 Human tra
32	1416.5	57.4	477	6	ABP96442	Abp96442 Mouse tra
33	1375.5	55.7	393	8	ADS11014	Adsl11014 Human the
34	1301	52.7	455	8	ADQ67776	Adq67776 Novel hum
35	1293.5	52.4	500	4	ABB76931	Abb76931 Rat VGL
36	1263	51.2	263	6	ABU52589	Abu52589 Human NOV
37	1263	51.2	322	8	ADS12237	Adsl12237 Human the
38	1263	51.2	322	8	ADS12238	Adsl12238 Human the
39	1255.5	50.9	485	6	ABB99355	Abb99355 Amino aci
40	1255.5	50.9	485	7	ADD37511	Add37511 Human tra
41	1255.5	50.9	485	10	AEF18856	Aef18856 Human Ami
42	1255.5	50.9	504	4	AAm38898	Aam38898 Human pol
43	1255.5	50.9	504	7	ADN95120	Adn95120 Human LEC
44	1255.5	50.9	516	4	AAm40684	Aam40684 Human pol
45	1252.5	50.7	476	4	AAE04910	Aae04910 Human tra

ALIGNMENTS

RESULT 1
ADF90164
ID ADF90164 standard; protein; 476 AA.
XX
AC ADF90164;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human transporter protein.
XX
KW peptide therapy; human; transporter.
XX
OS Homo sapiens.
XX
PN US2003170778-A1.
XX
PD 11-SEP-2003.
XX
PF 14-MAR-2001; 2001US-00805456.
XX
PR 22-DEC-2000; 2000US-0257175P.
XX
PA (WEIM/) WEI M.
PA (YANC/) YAN C.
PA (MERK/) MERKLOV G V.
PA (KEFC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
XX
PI Wei M, Yan C, Merklov GV, Ketchum KA, Di Francesco V, Beasley EM;
XX
DR WPI; 2003-898259/82.
XX
N-PSDB; ADF90163.
XX
PT New human transporter peptide, useful for preparing a composition for
XX
PS treating a disease or condition mediated by human transporters.
XX
PT Claim 1; SEQ ID NO 2; 94pp; English.
XX
PS The invention describes an isolated peptide comprising a 476 amino acid
XX
CC sequence (S1) or its allelic variant, orthologue or fragment, where the
XX
CC allelic variant or orthologue is encoded by a nucleic acid that
XX
CC hybridises under stringent conditions to the opposite strand of a nucleic
XX
CC acid comprising a sequence having 2093 or 46649 base pairs, and the
XX
CC fragment comprises 10 contiguous amino acids of S1. The peptide is useful
XX
CC for preparing a composition for treating a disease or condition mediated

CC by a human transporter protein. This is the amino acid sequence of a
CC human transporter protein.
XX
SQ Sequence 476 AA;

Query Match 100.0%; Score 2469; DB 7; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.4e-258;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTQRLNEDYHDYSDTSPSPSEGLNLSPGSYQRFQGSNSTTWFTQTLIHLKGN 60
Db 1 MSTQRLNEDYHDYSDTSPSPSEGLNLSPGSYQRFQGSNSTTWFTQTLIHLKGN 60
Qy 61 IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRLNKSFDYGDV 120
Db 61 IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRLNKSFDYGDV 120
Qy 121 MYGLESPCSWLNHAHWGRVVDFFLIIVTQLGCCVYFVLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSWLNHAHWGRVVDFFLIIVTQLGCCVYFVLADNFKQVIEAANGTTNNC 180
Qy 181 HNNETVILPTMDSRLYMLSFPLVLLVFIIRNLRLSIFSLLANITMLVSLVMYQFIV 240
Db 181 HNNETVILPTMDSRLYMLSFPLVLLVFIIRNLRLSIFSLLANITMLVSLVMYQFIV 240
Qy 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPKRPFLILYLGWVIT 300
Db 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPKRPFLILYLGWVIT 300
Qy 301 ILVISLGLYLOFGANIQSITLNLPCWLYQSVKLLYSIGIFFFTVALQFYVPAEIIIP 360
Db 301 ILVISLGLYLOFGANIQSITLNLPCWLYQSVKLLYSIGIFFFTVALQFYVPAEIIIP 360
Qy 361 FFVSRAPHECELVDLFRVTVLVCILAILPRDLVLSVGSVSSSALALIIPPLE 420
Db 361 FFVSRAPHECELVDLFRVTVLVCILAILPRDLVLSVGSVSSSALALIIPPLE 420
Qy 421 VTTFYSEGMSPLTIFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476
Db 421 VTTFYSEGMSPLTIFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476

RESULT 2
ADRO3799
ID ADRO3799 standard; protein; 476 AA.
XX
AC ADRO3799;
XX
XX 21-OCT-2004 (first entry)
XX
XX Human novel transporter protein.
XX
XX Human; chromosome 5; transporter.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 431..432
XX /note= "Encoded by CCCCCTC (SEQ ID 3 only)"
XX
XX US2004146887-A1.
XX
XX 29-JUL-2004.
XX
XX 07-OCT-2003; 2003US-00679362.
XX
XX 22-DEC-2000; 2000US-0257175P.
XX 14-MAR-2001; 2001US-00805456.
XX
XX (APPL-) APPLERA CORP.
XX
XX Wei M, Yan C, Merklov G, Ketchum KA, Difrancesco V, Beasley EM;
XX

DR
DR N-PSDB; ADR03798, ADR03800.
XX
XX New nucleic acid encoding human transporter peptides, useful for
PT preparing agents for treating a disease or condition mediated by human
PT transporters.
XX
XX Claim 12; SEQ ID NO 2; 62pp; English.
XX
XX The invention relates to a new isolated nucleic acid comprising a
CC sequence encoding a transporter protein (appearing as ADR03799) and
CC appearing as ADR03798 (the cDNA) or ADR03800 (the gene). Also included
CC are a vector comprising the isolated nucleic acid, a host cell containing
CC the vector, producing the polypeptide, detecting the presence of the
CC nucleic acid in a sample and an isolated human peptide having a sequence
CC that shares at least 70% homology with ADR03799. The gene encoding the
CC human transporter is located on chromosome 5. The peptide is useful for
CC preparing agents for treating a disease or condition mediated by a human
CC transporter protein. The present sequence represents the transporter
CC protein.
XX
SQ Sequence 476 AA;

Query Match 100.0%; Score 2469; DB 8; Length 476;
Best Local Similarity 100.0%; Pred. No. 7.4e-258;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTQRLNEDYHDYSDTSPSPSEGLNLSPGSYQRFQGSNSTTWFTQTLIHLKGN 60
Db 1 MSTQRLNEDYHDYSDTSPSPSEGLNLSPGSYQRFQGSNSTTWFTQTLIHLKGN 60
Qy 61 IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRLNKSFDYGDV 120
Db 61 IGTGLLGLPLAVKNAGIVMGPISLLIIGIVAVHCMGILVKCAHHFCRLNKSFDYGDV 120
Qy 121 MYGLESPCSWLNHAHWGRVVDFFLIIVTQLGCCVYFVLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSWLNHAHWGRVVDFFLIIVTQLGCCVYFVLADNFKQVIEAANGTTNNC 180
Qy 181 HNNETVILPTMDSRLYMLSFPLVLLVFIIRNLRLSIFSLLANITMLVSLVMYQFIV 240
Db 181 HNNETVILPTMDSRLYMLSFPLVLLVFIIRNLRLSIFSLLANITMLVSLVMYQFIV 240
Qy 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPKRPFLILYLGWVIT 300
Db 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPKRPFLILYLGWVIT 300
Qy 301 ILVISLGLYLOFGANIQSITLNLPCWLYQSVKLLYSIGIFFFTVALQFYVPAEIIIP 360
Db 301 ILVISLGLYLOFGANIQSITLNLPCWLYQSVKLLYSIGIFFFTVALQFYVPAEIIIP 360
Qy 361 FFVSRAPHECELVDLFRVTVLVCILAILPRDLVLSVGSVSSSALALIIPPLE 420
Db 361 FFVSRAPHECELVDLFRVTVLVCILAILPRDLVLSVGSVSSSALALIIPPLE 420
Qy 421 VTTFYSEGMSPLTIFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476
Db 421 VTTFYSEGMSPLTIFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476

RESULT 3
ABG75834
ID ABG75834 standard; protein; 507 AA.
XX
XX AC ABG75834;
XX
XX 10-MAY-2003 (first entry)
XX
XX DE Transporters and ion channels protein 16, TRICH-16.
XX
XX Human; transporter and ion channel; TRICH; Gene therapy;
XX cell proliferative disorder; transport disorder; neurological disorder;
XX muscle disorder; immunological disorder; amyotrophic lateral sclerosis;
XX

KW cystic fibrosis; diabetes; Parkinson's disease; prostate cancer;
KW cardiac disorder; angina; Alzheimer's disease; amnesia; epilepsy;
KW schizophrenia; sickle cell anaemia; infertility; hyperglycaemia;
KW hypoglycaemia; hypercholesterolaemia; stroke; multiple sclerosis;
KW motor neuron disorder; prion disease; metabolic disease;
KW developmental disorder; central nervous system; cardiomyopathy;
KW hypertension; asthma; AIDS; allergy; anaemia; atherosclerosis;
KW atopic dermatitis; diabetes mellitus; osteoarthritis; osteoporosis;
KW rheumatoid arthritis; psoriasis; infection; trauma; hepatitis; cancer;
KW leukemia; lymphoma.
XX Homo sapiens.
OS
XX
XX WO2003016493-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 16-AUG-2002; 2002WO-US026323.
XX
XX PR 17-AUG-2001; 2001US-0313242P.
XX PR 21-SEP-2001; 2001US-0324782P.
XX PR 02-OCT-2001; 2001US-0328184P.
XX PR 26-OCT-2001; 2001US-0345937P.
XX PR 01-NOV-2001; 2001US-0335698P.
XX PR 13-NOV-2001; 2001US-0332804P.
XX PR 27-NOV-2001; 2001US-0333922P.
XX PR 26-APR-2002; 2002US-0375637P.
XX PR 03-MAY-2002; 2002US-0377444P.
XX PR 11-JUN-2002; 2002US-0388180P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX
XX PI Tang YT, Lal PG, Yue H, Baughn MR, Nguyen DB, Yao MG, Greene BD;
PI Borowsky ML, Lee S, Emerling BM, Xu Y, Becha SD, Corvad AE;
PI Azimzai Y, Lee H, Elliott VS, Lee EA, Yang J, Lehr-Mason FM;
PI Rankumar J, Lee SY, Faris M, Turner C, Furness M, Buchbinder JL;
PI Walia NK, Li JX, Forsythe IJ, Griffin JA, Gietzen KJ, Swarnakar A;
PI Hafalia AJA, Lindquist EA, Jiang X, Jackson AA, Wilson AD, Jin P;
PI Khare R, Marquis JP;
XX
XX WPI; 2003-268319/26.
DR N-PSDB; ABX12019.
XX
XX PT Novel human transporter and ion channel polypeptides and polynucleotides
PT for diagnosing, preventing or treating cell proliferative, transport,
PT neurological, muscle and immunological disorders.
XX
XX PS -Claim 1; Page 216-217; 253pp; English.
XX
XX The invention discloses isolated polypeptides chosen from human
CC transporter and ion channel polypeptides, TRICH 1-26, a biologically
CC active or immunogenic fragment and the nucleic acids encoding them. Also
CC disclosed are isolated antibodies raised against the TRICH proteins.
CC methods for detecting a target polynucleotide in a sample and a
CC microarray where at least one element is a TRICH polynucleotide. The
CC proteins are useful for screening for agonists or antagonists, which can
CC then be used for treating a disease or condition associated with
CC decreased or overexpression of functional TRICH in a patient, for
CC screening for a compound that modulates the activity of the polypeptide
CC or that binds to the polypeptide or as an immunogen for preparing
CC antibodies. The polynucleotides are useful for screening for compounds
CC which alter expression of a target polynucleotide or for assessing
CC toxicity of a test compound. The polypeptides, polynucleotides,
CC modulators and antibodies are useful for diagnosis, treatment (e.g. gene
CC therapy) and prevention of cell proliferative, transport, neurological,
CC muscle and immunological disorders, such as amyotrophic lateral
CC sclerosis, cystic fibrosis, diabetes, Parkinson's disease, prostate
CC cancer, cardiac disorders, angina, Alzheimer's disease, amnesia,
CC epilepsy, schizophrenia, sickle cell anaemia, infertility,
CC hyperglycaemia, hypoglycaemia, hypercholesterolaemia, stroke, multiple
CC sclerosis, motor neuron disorder, prion disease, metabolic disease of the
CC nervous system, developmental disorders of the central nervous system,
CC cardiomyopathy, hypertension, asthma, AIDS, allergies, anaemia,

CC atherosclerosis, atopic dermatitis, diabetes mellitus, osteoarthritis,
CC osteoporosis, rheumatoid arthritis, psoriasis, infections, trauma,
CC hepatitis and cancers, including leukemia and lymphoma. The sequences
CC presented in ABG75819-ABG75844 are the TRICH proteins of the invention
XX
SQ Sequence 507 AA;
Query Match 99.9%; Score 2466; DB 6; Length 507;
Best Local Similarity 99.8%; Pred. NO. 1.7e-257;
Matches 475; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTQRLRNEDYHDYSSSTDVSPESPSEGNNLSSPGSYQRFQSNSTTFQTLHLKGN 60
DB :|||||
32 LSTQRLRNEDYHDYSSSTDVSPESPSEGNNLSSPGSYQRFQSNSTTFQTLHLKGN 91
QY 61 IGTGLLGLPLAVKXAGIWMGPISILLIIGIVAVHCNGLVKCAHFCRRLNKSFVDYGDIV 120
DB :|||||
92 IGTGLLGLPLAVKXAGIWMGPISILLIIGIVAVHCNGLVKCAHFCRRLNKSFVDYGDIV 151
QY 121 MYGLESSPCSWLRNHAHWRVDFFLIVTQGFCCVYFVLADNFKQVIEAANGTTNNC 180
DB :|||||
152 MYGLESSPCSWLRNHAHWRVDFFLIVTQGFCCVYFVLADNFKQVIEAANGTTNNC 211
QY 181 HNNETVILTPMDSRLYMLSELPFLVLLVFNRLPALSIFSLLANITMLVSLWMIYQFIV 240
DB :|||||
212 HNNETVILTPMDSRLYMLSELPFLVLLVFNRLPALSIFSLLANITMLVSLWMIYQFIV 271
QY 241 QRIIDPDSHLPLVAPWKTYPLFFGTAFSFEGLGMVLPLENKMKDKPRKPLIILYGLWVI 300
DB :|||||
272 QRIIDPDSHLPLVAPWKTYPLFFGTAFSFEGLGMVLPLENKMKDKPRKPLIILYGLWVI 331
QY 301 ILXISLGLCYLQFGANIQGSITLNLPCNWLQSVKLLYSIGIFFTYALQFYVPAEIIIP 360
DB :|||||
332 ILXISLGLCYLQFGANIQGSITLNLPCNWLQSVKLLYSIGIFFTYALQFYVPAEIIIP 391
QY 361 FFVSRAPHCHELVDLDFVTVLVLCITLAILPRLDLVISLVGSSSALALIIPPLLE 420
DB :|||||
392 FFVSRAPHCHELVDLDFVTVLVLCITLAILPRLDLVISLVGSSSALALIIPPLLE 451
QY 421 VTFYSEGMSPLTTFKDALISILGFGVGVGTGYEALYELIOPSNAPIFINSTCAFI 476
DB :|||||
452 VTFYSEGMSPLTTFKDALISILGFGVGVGTGYEALYELIOPSNAPIFINSTCAFI 507
RESULT 4
ABP96441
ID ABP96441 standard; protein; 476 AA.
XX
XX AC ABP96441;
XX
XX DT 02-JUN-2003 (first entry)
XX
XX DE Human tranndorin 3 protein SEQ ID NO:21.
KW Neuroprotective; nootropic; cerebroprotective; analgesic; gene therapy;
KW central nervous system disorder; CNS disorder; multiple sclerosis;
KW nerve injury; neuropathic pain; stroke; trauma; non-CNS disorder; tramdi;
KW tranndorin; human; tramndorin 3; chromosome 5.
XX Homo sapiens.
XX
XX FH Key Location/Qualifiers
FT Misc-difference 356 /note= "encoded by GAG"
XX
XX PN WO2003016502-A2.
XX
XX PD 27-FEB-2003.
XX
XX PF 21-AUG-2002; 2002WO-US026637.
XX
XX PR 21-AUG-2001; 2001US-0313907P.
XX PR 21-AUG-2002; 2002US-00225810.

XX PA	(MCLA-) MCLAUGHLIN RES INST.	DT	04-MAR-2003 (first entry)	XX
XX PI	Birmingham JR;	XX DE	Human NOVX protein, NOV7b.	XX
XX PI		XX KW	Human; immunogen; NOVX; metabolic disorder; diabetes; cardiomyopathy;	XX
XX PI		XX KW	obesity; infectious disease; anorexia; neurodegenerative disorder;	XX
DR DR	WPI; 2003-278567/27.	XX KW	Alzheimer's disease; Parkinson's disease; immune disorder;	XX
DR DR	N-PSDB; ABZ80236.	XX KW	haematopoietic disorder; dyslipidaemia; metabolic disturbance;	XX
XX PT	New nucleic acid sequence encoding tramdorins, e.g. mouse tramd 1, mouse	XX OS	metabolic syndrome X; wasting disorder; cancer; gene therapy.	XX
XX PT	tramd 2, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or	XX XX	Homo sapiens.	XX
XX PT	rat tramd 1, useful for treating CNS, e.g. stroke, multiple sclerosis,	XX PN	WO200281518-A2.	XX
XX PT	trauma, neuropathic pain.	XX PD	17-OCT-2002.	XX
XX PS	Example 11; Fig 21; 177pp; English.	XX PF	21-FEB-2002; 2002WO-US005374.	XX
XX CC	The present invention describes an isolated nucleic acid sequence	XX PR	21-FEB-2001; 2001US-0270220P.	XX
XX CC	comprising a cDNA sequence encoding mouse tramdorin (tramd) 2, mouse	XX PR	21-FEB-2001; 2001US-0270523P.	XX
XX CC	tramd 3, human tramd 1, human tramd 2, human tramd 3 or rat tramd 1, or	XX PR	23-FEB-2001; 2001US-0270797P.	XX
XX CC	the genomic sequence of mouse tramd 1 or mouse tramd 3. Mouse tramd 1 is	XX PR	23-FEB-2001; 2001US-0270810P.	XX
XX CC	located to chromosome 11, whereas human tramd 1 is located to chromosome	XX PR	08-MAR-2001; 2001US-0274295P.	XX
XX CC	-5q31-33. The tramd sequences have neuroprotective, nootropic, analgesic	XX PR	16-MAR-2001; 2001US-0276400P.	XX
XX CC	and cerebroprotective activities, and can be used in gene therapy. The	XX PR	16-MAR-2001; 2001US-0276877P.	XX
XX CC	nucleic acid sequences are useful for diagnosing and treating central	XX PR	26-MAR-2001; 2001US-0278796P.	XX
XX CC	nervous system (CNS) disorders such as multiple sclerosis, nerve injury,	XX PR	04-APR-2001; 2001US-0281521P.	XX
XX CC	neuropathic pain, stroke or trauma, and non-CNS disorders. The present	XX PR	25-APR-2001; 2001US-0286548P.	XX
XX CC	sequence represents human tramd 3, which is given in the exemplification	XX PR	17-MAY-2001; 2001US-0291765P.	XX
XX CC	of the present invention	XX PR	10-AUG-2001; 2001US-0311595P.	XX
XX SQ	Sequence 476 AA;	XX PR	13-AUG-2001; 2001US-0311980P.	XX
		XX PR	10-SEP-2001; 2001US-0318526P.	XX
		XX PR	17-SEP-2001; 2001US-0322712P.	XX
		XX PR	18-OCT-2001; 2001US-0330307P.	XX
		XX PA	(CURA-) CURAGEN CORP.	XX
QY	Query Match 99.7%; Score 2461; DB 6; Length 476;	XX PI	Pena CEA, Shinkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA;	XX
DB	Best Local Similarity 99.8%; Pred. No. 5.5e-257;	XX PI	Vernet CAM, Malyankar UL, Guo X, Gusev VY, Casman SU, Boldog FL;	XX
	Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	XX PI	Furtak K, Tchernev VT, Patturajan M, Gangolli EA, Padigaru M, Liu X;	XX
		XX PI	Baumgartner JC, Gerlach VL, Spaderna SK, Zerhusen BD;	XX
QY	1 MSTORLNEDYHYSSTDVSPESPSGLNMLSPGSYQRFQSGNSTTWFQTLHLKGN 60	XX DR	WPI; 2003-046859/04.	XX
DB	1 MSTORLNEDYHYSSTDVSPESPSGLNMLSPGSYQRFQSGNSTTWFQTLHLKGN 60	XX DR	N-PSDB; ABX70643.	XX
QY	61 IGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHCHWGLVKCAHHFCRLNKSFDYDGTV 120	XX PT	New isolated NOVX polypeptide useful for treating cardiomyopathy,	XX
DB	61 IGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHCHWGLVKCAHHFCRLNKSFDYDGTV 120	XX PT	atherosclerosis, metabolic disorders, diabetes, obesity, infectious	XX
QY	121 MYGLESPCSMLRNHAWHGRVVDFFLIVTQLGFCVYFVLADNFKQVIEAANGTTNNC 180	XX PT	disease, anorexia, neurodegenerative disorders, Alzheimer's disease and	XX
DB	121 MYGLESPCSMLRNHAWHGRVVDFFLIVTQLGFCVYFVLADNFKQVIEAANGTTNNC 180	XX PT	cancer.	XX
QY	181 HNNETVILTPMDSRLYMLFPLVLLVTRNLRLSIFSLANITMLVSLVMYQFIV 240	XX PS	Claim 1; Page 57; 479pp; English.	XX
DB	181 HNNETVILTPMDSRLYMLFPLVLLVTRNLRLSIFSLANITMLVSLVMYQFIV 240	XX PS	The invention relates to an isolated polypeptide termed NOVX (NOV1, 2a,	XX
QY	241 QRIPDPSHLPLVAPWKTYPIFFGTAFISFEGIGMVLPLENKMKDPKRFPLILYLGWVIT 300	XX CC	2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15,	XX
DB	241 QRIPDPSHLPLVAPWKTYPIFFGTAFISFEGIGMVLPLENKMKDPKRFPLILYLGWVIT 300	XX CC	16a-d, 17a-b, 18, 19, 20a-b, 21-30) appearing as ABU52578-ABU52624), a	XX
QY	301 ILYSISGLCYLQPGANIQSITLNPNCMLYQSVKLLYSIGIFFTVALQFYVPAEIIIP 360	XX CC	variant of NOVX, a mature form of NOVX, and a variant of the mature form	XX
DB	301 ILYSISGLCYLQPGANIQSITLNPNCMLYQSVKLLYSIGIFFTVALQFYVPAEIIIP 360	XX CC	of NOVX. Also included are a nucleic acid molecule (NOVX NA) encoding	XX
QY	361 FFVSRAPHELCVLVDLVRVTVLCTCILAILIPLRLDLVLSVGSVSSALALIIPLE 420	XX CC	NOVX, or a fragment or complement of NOVX NA, a vector comprising NOVX	XX
DB	361 FFVSRAPHELCVLVDLVRVTVLCTCILAILIPLRLDLVLSVGSVSSALALIIPLE 420	XX CC	NA, a cell comprising the vector, an anti-NOVX antibody (ab), determining	XX
QY	421 VTFYSGMSPLTIFFKDALISILGFGVFGVTGYEALYELIQPSNAPFINSTCAFI 476	XX CC	the presence or amount of NOVX or NOVX NA in a sample, and identifying an	XX
DB	421 VTFYSGMSPLTIFFKDALISILGFGVFGVTGYEALYELIQPSNAPFINSTCAFI 476	XX CC	agent that binds or modulates the expression or activity of NOVX. NOVX,	XX
		XX CC	NOVX NA or ab is useful for treating or preventing a NOVX-associated	XX
		XX CC	disorder in a subject, preferably human. Ab is useful for determining the	XX
		XX CC	presence or amount of NOVX in a sample. NOVX is useful for identifying an	XX
		XX CC	agent that binds to NOVX. NOVX, NOVX NA or ab is useful for treating	XX
		XX CC	metabolic disorders, diabetes, cardiomyopathy, obesity, infectious	XX
		XX CC	disease, anorexia, neurodegenerative disorders, Alzheimer's disease,	XX
		XX CC	Parkinson's disease, immune disorders, haematopoietic disorders, and	XX
		XX CC	various dyslipidaemias, metabolic disturbances associated with obesity,	XX
		XX CC	the metabolic syndrome X and wasting disorders associated with chronic	XX
		XX CC	diseases, various cancers, endocrine, connective tissue, blood, vascular,	XX
		XX CC	skin, renal, bone, brain, muscle disorders, or bacterial, fungal,	XX
		XX CC	protozoal or viral infections. NOVX, NOVX NA or ab is useful in screening	XX
RESULT 5				
ABU52588				
ID	ABU52588 standard; protein; 496 AA.			
XX				
AC	ABU52588;			
XX				

assays, detection assays, predictive medicine, and in methods of treatment. NOVX is useful as immunogen, to screen for potential antagonist/agonist compounds, and as bait protein in a two-hybrid or three-hybrid assay. NOVX NA is useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX activity. The cell is useful for producing non-human transgenic animals. Ab is useful for isolating, and purifying NOVX and to monitor protein levels in tissue as part of a clinical testing procedure. The present sequence represents a NOVX protein

Sequence 496 AA;

Query Match 99.6% Score 2460 DB 6 Length 496;

Best Local Similarity 99.8%; Pred. No. 7.4e-257;

Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MSTORL	RNEDYH	YSS	TDVS	PEESP	EGNN	MLSS	PGSY	QRFG	QSNT	TWFQ	TLL	HL	KG	60
Db	21	MSTORL	RNEDYH	YSS	TDVS	PEESP	EGNN	MLSS	PGSY	QRFG	QSNT	TWFQ	TLL	HL	KG	80
Qy	61	IGTGL	LGLP	LAV	KNAGI	VMG	PI	SLLI	IIG	IVAV	HC	MLV	KCAH	HF	CR	LNKS
Db	81	IGTGL	LGLP	LAV	KNAGI	VMG	PI	SLLI	IIG	IVAV	HC	MLV	KCAH	HF	CR	LNKS
Qy	121	MYG	LESS	PC	SW	RN	HAH	WGR	R	V	D	P	F	L	I	180
Db	141	MYG	LESS	PC	SW	RN	HAH	WGR	R	V	D	P	F	L	I	200
Qy	181	HN	NET	V	I	L	T	P	T	M	D	S	R	L	Y	240
Db	201	HN	NET	V	I	L	T	P	T	M	D	S	R	L	Y	260
Qy	241	QRI	P	D	P	S	H	L	P	L	V	A	P	K	M	300
Db	261	QRI	P	D	P	S	H	L	P	L	V	A	P	K	M	320
Qy	301	I	L	Y	I	S	L	G	C	G	I	Q	F	O	R	360
Db	321	I	L	Y	I	S	L	G	C	G	I	Q	F	O	R	380
Qy	361	F	F	V	S	R	A	P	E	C	H	L	V	D	L	420
Db	381	F	F	V	S	R	A	P	E	C	H	L	V	D	L	440
Qy	421	V	T	T	F	Y	S	E	G	M	S	P	L	T	I	476
Db	441	V	T	T	F	Y	S	E	G	M	S	P	L	T	I	496

RESULT 6

RESUL 6
AAO14191

AAO14191 standard: protein: 568 AA:

AAO14191:

DT 03-MAY-2002 (first entry)

XX Human transporter and ion channel TRPCH-8

XX Human; transporter and ion channel; TRICH; transport disorder;
KW neurological disorder; muscle disorder; immunological disorder;
KW cell proliferative disorder; neuroprotective; nootropic;
KW cerebroprotective; immunosuppressive; cytostatic; respiratory; muscular;
KW gene therapy.

Homo sapiens.

PN WO200204520-A2

17-JAN-2002

XX
DE 05-JUN-2001. 2001WC-IIS031448XX
34

PR	07-JUL-2000; 2000US-0216547P.	
PR	14-JUL-2000; 2000US-0218232P.	
PR	21-JUL-2000; 2000US-0220112P.	
PR	28-JUL-2000; 2000US-0221839P.	
XX		
XX	(INCY-) INCYTE GENOMICS INC.	
PA		
XX		
PI	Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;	
PI	Burford N, Greene BD, Sanjanwala MS, Baughn MR, Yao MG, Yang J;	
PI	Patterson C, Gandhi AR, Hafalia AJA, Tribouley CM, Walia NK;	
PI	Ali-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DAM, Azimzai Y, Lal P;	
PI	Elliot V, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan FA;	
PI	Kearney L, Thangavelu K, Das D, Policky JL;	
XX		
XX	WPI; 2002-205969/26.	
DR	N-PSDB; AAL44674.	
XX		
PT	New human transporters and ion channel polypeptides for diagnosing,	
PT	treating or preventing transport, neurological; muscle, immunological and	
PT	cell proliferative disorders.	
XX		
XX	Claim 1; Page 155-156; 230pp; English.	
PS		
XX		
CC	The present invention provides the protein and coding sequences of a	
CC	number of human transporter and ion channel proteins, designated TRICH-1-	
CC	TRICH-32. The sequences can be used in the treatment of transport,	
CC	neurological, muscle, immunological and cell proliferative disorders. The	
CC	present sequence is a protein of the invention	
XX		
XX	sequence 568 AA;	
SQ		

Query Match 97.3%; Score 2402.5; DB 5; Length 568;

Best Local Similarity 88.3%; Pred. No. 1.5e-250;

Mismatches	61;	Gaps	2;
Indels	2;		
Mismatches	0;		
Conservative	474;		
Matches	61;	Gaps	2;

[illegible]

RESULT. T 7

ABU52587
 ID ABU52587 standard; protein; 500 AA.
 XX
 AC ABU52587;
 DT
 DT 04-MAR-2003 (first entry)
 XX
 DE Human NOVX protein, NOV7a.
 XX
 KW Human; immunogen; NOVX; metabolic disorder; diabetes; cardiomyopathy;
 KW obesity; infectious disease; anorexia; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; immune disorder;
 KW hematopoietic disorder; dyslipidaemia; metabolic disturbance;
 KW metabolic syndrome X; wasting disorder; cancer; gene therapy; SNP;
 KW single nucleotide polymorphism.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 173
 FT /note= "May be Val as a result of a single nucleotide
 FT polymorphism"
 XX
 PN WO200281518-A2.
 XX
 PD *17-OCT-2002.
 XX
 PF 21-FEB-2002; 2002WO-US005374.
 XX
 PR 21-FEB-2001; 2001US-0270220P.
 PR 21-FEB-2001; 2001US-0270523P.
 PR 23-FEB-2001; 2001US-0270797P.
 PR 23-FEB-2001; 2001US-0270810P.
 PR 08-MAR-2001; 2001US-0274295P.
 PR 16-MAR-2001; 2001US-0276400P.
 PR 16-MAR-2001; 2001US-0276677P.
 PR 26-MAR-2001; 2001US-0278796P.
 PR 04-APR-2001; 2001US-0281521P.
 PR 25-APR-2001; 2001US-0286548P.
 PR 17-MAY-2001; 2001US-0291765P.
 PR 10-AUG-2001; 2001US-0311595P.
 PR 11-AUG-2001; 2001US-0311980P.
 PR 10-SEP-2001; 2001US-0318526P.
 PR 17-SEP-2001; 2001US-0322712P.
 PR 18-OCT-2001; 2001US-0330307P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Pena CE, Shinkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA;
 PI Vernet CAM, Malyankar UL, Guo X, Gusev VY, Casman SJ, Boidog FL;
 PI Furtak K, Tchernev VT, Patturajan M, Gangolli EA, Padigar M, Liu X;
 PI Baumgartner JC, Gerlach VL, Spaderna SK, Zerhusen BD;
 XX
 XX WPI; 2003-046859/04.
 DR N-PSDB; ABX70642.
 XX
 XX New isolated NOVX polypeptide useful for treating cardiomyopathy,
 PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
 PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
 PT cancer.
 XX
 PS Claim 1; Page 56; 479pp; English.
 XX
 CC The invention relates to an isolated polypeptide termed NOVX (NOV1, 2a,
 CC 2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15,
 CC 16a-d, 17a-b, 18, 19, 20a-b, 21-30) appearing as ABU52578-ABU52624), a
 CC variant of NOVX, a mature form of NOVX, and a variant of the mature form
 CC of NOVX. Also included are a nucleic acid molecule (NOVX NA) encoding
 CC NOVX, or a fragment or complement of NOVX NA, a vector comprising NOVX
 CC NA, a cell comprising the vector, an anti-NOVX antibody (ab), determining
 CC the presence or amount of NOVX or NOVX NA in a sample, and identifying an
 CC agent that binds or modulates the expression or activity of NOVX. NOVX,
 CC NOVX NA or ab is useful for treating or preventing a NOVX-associated

CC disorder in a subject, preferably human. Ab is useful for determining the
 CC presence or amount of NOVX in a sample. NOVX is useful for identifying an
 CC agent that binds to NOVX. NOVX, NOVX NA or ab is useful for treating
 CC metabolic disorders, diabetes, cardiomyopathy, obesity, infectious
 CC disease, anorexia, neurodegenerative disorders, Alzheimer's disease,
 CC Parkinson's disease, immune disorders, haematopoietic disorders, and
 CC various dyslipidaemias, metabolic disturbances associated with obesity,
 CC the metabolic syndrome X and wasting disorders associated with chronic
 CC diseases, various cancers, endocrine, connective tissue, blood, vascular,
 CC skin, renal, bone, brain, muscle disorders, or bacterial, fungal,
 CC protozoal or viral infections. NOVX, NOVX NA or ab is useful in screening
 CC assays, detection assays, predictive medicine, and in methods of
 CC treatment. NOVX is useful as immunogen, to screen for potential
 CC ant/agonist compounds, and as bait protein in a two-hybrid or three-
 CC hybrid assay. NOVX NA is useful in gene therapy, to express NOVX, to
 CC detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX
 CC activity. The cell is useful for producing non-human transgenic animals.
 CC Ab is useful for isolating, and purifying NOVX and to monitor protein
 CC levels in tissue as part of a clinical testing procedure. The present
 CC sequence represents a NOVX protein
 XX
 SQ Sequence 500 AA;
 Query Match 97.1%; Score 2398; DB 6; Length 500;
 Best Local Similarity 97.5%; Pred. No. 3.9e-250;
 Matches 472; Conservative 0; Mismatches 0; Indels 12; Gaps 3;
 QY 1 MSTQRLRNEDYHDYSDTSDVSPESPSEGLNLSPGSYQRFQGSNSTTWFTQLHLKGN 60
 DB 21 MSTQRLRNEDYHDYSDTSDVSPESPSEGLNLSPGSYQRFQGSNSTTWFTQLHLKGN 80
 QY 61 IGTGLLGLPLAVKNAGIVMGPIISLLIIGIVAVHMGILVKCAHFCRLNKSFVDYGDIV 120
 DB 81 IGTGLLGLPLAVKNAGIVMGPIISLLIIGIVAVHMGILVKCAHFCRLNKSFVDYGDIV 140
 QY 121 MYGLESPCSWLRNHAHNGRRVVDFFLIYVTLQGFCCVYFVFLADNFKQVIEAANGTTNCC 180
 DB 141 MYGLESPCSWLRNHAHNGRRVVDFFLIYVTLQGFCCVYFVFLADNFKQVIEAANGTTNCC 200
 QY 181 HNNETVILPTMDSRLYMLSFPLVLLVFNRLRLAISFLLANITMLVSLVMYQFIV 240
 DB 201 HNNETVILPTMDSRLYMLSFPLVLLVFNRLRLAISFLLANITMLVSLVMYQFIV 260
 QY 241 -----QRIPDPHPLVAPWKTYPLPFGTAIFSPFEGIGMVLPLENKKDKPRKPLIL 292
 DB 261 FRYMLSVFORIPDPHPLVAPWKTYPLPFGTAIFSPFEGIGMVLPLENKKDKPRKPLIL 320
 QY 293 YLGMVITVITLYISLGLGVLOFGANIOGSIITNLNPNCLYQSVKLLYSIGIFFTYALQFY 352
 DB 321 YLGMVITVITLYISLGLGVLOFGANIOGSIITNLNPNCLYQSVKLLYSIGIFFTYALQFY 377
 QY 353 VPAEIIIPFVSRAPCHCELVDLFRVTVLVCLTCLIAILIPRLDLVISLVGVSSSALA 412
 DB 378 VPAEIIIPFVSRAPCHCELVDLFRVTVLVCLTCLIAILIPRLDLVISLVGVSSSALA 436
 QY 413 LIIPPLEVTTFYSEGMSPLTIFKDALISILGFVGVFGVYEALEYLIQPSNAPIFINST 472
 DB 437 LIIPPLEVTTFYSEGMSPLTIFKDALISILGFVGVFGVYEALEYLIQPSNAPIFINST 496
 QY 473 CAFI 476
 DB 497 CAFI 500
 RESULT 8
 ABB76941
 ID ABB76941 standard; protein; 476 AA.
 XX
 AC ABB76941;
 XX
 DT 22-JUL-2002 (first entry)
 XX
 DE Human VG51.

XX Antiasthmatic; anxiolytic; antiepileptic; antihypertensive; human;
KW psychotropic; glutamate transporter; transporter; GABA;
KW gamma-aminobutyric acid transporter; GABA transporter; neurotransmitter;
KW asthma; anxiety; epilepsy; hypertension; psychiatric disorder;
KW neurotic disorder; VG51.
XX
OS Homo sapiens.
XX
XX WO200071709-A1.
XX
XX 30-NOV-2000.
XX
XX 19-MAY-2000; 2000WO-FR001383.
XX
XX 21-MAY-1999; 99FR-00006525.
XX
XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX
XX Giros B, Gasnier B, Sagne C, El Mestikawy S, Hamon M;
XX
XX WPI; 2001-025160/03.
XX
XX N-PSDB; ABL57930.
XX
XX New mammalian amino acid transporter, used e.g. to screen for
XX psychotropic agents, is high capacity but low affinity transporter of
XX gamma-aminobutyric acid.
XX
XX Claim 2; Fig 13; 103pp; French.
XX
XX The present sequence is the protein sequence for human VG51, a glutamate/
XX gamma-aminobutyric acid (GABA) transporter. GABA and glutamate are
XX neurotransmitters. The transporter can be used to produce specific
XX antibodies, to screen for binding agents. Modulators of the transporter
XX are useful for treating disorders associated with deregulated
XX glutamate/GABA transport, e.g. asthma, anxiety, epilepsy, hypertension
XX and other psychiatric and neurotic disorders, while determining levels of
XX the transporter and its coding sequence can be used for diagnosis of such
XX disorders
XX
XX Sequence 476 AA;
SQ
Query Match 94.1%; Score 2324; DB 4; Length 476;
Best Local Similarity 94.5%; Pred. No. 3.8e-242;
Matches 450; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
Qy 1 MSTQRLNEDYHDSSTDVSPSESGLNLSPPSGSYQRFQGSNTTWFQTLIHLKGN 60
Db 1 MSTQRLNEDYHDSSTDVSPSESGLNLSPPSGSYQRFQGSNTTWFQTLIHLKGN 60
Qy 61 IGTGLGLPLAVKAGIWMGPISLLIIGIVAVHGMGILVKAHFCRLNKSFDYDGTIV 120
Db 61 IGTGLGLPLAVKAGIWMGPISLLIIGIVAVHGMGILVKAHFCRLNKSFDYDGTIV 120
Qy 121 MYGLESPCSWLNRHAGRWVDFLLVITQFGCCVYFVLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSWLNRHAGRWVDFLLVITQFGCCVYFVLADNFKQVIEAANGTTNNC 180
Qy 181 HNNETVILPTMTDSRLYMLSPFLPLVLLVFIRNLRALSIFSLANITMLVSLVMYQFIV 240
Db 181 HNNETVILPTMTDSRLYMLSPFLPLVLLVFIRNLRALSIFSLANITMLVSLVMYQFIV 240
Qy 241 QRIIDPSHLPLVAPWKTYPFEGTAIFSEFEGIMVLPLENKMDPRKPEPLIYLGMVIT 300
Db 241 QRIIDPSHLPLVAPWKTYPFEGTAIFSEFEGIMVLPLENKMDPRKPEPLIYLGMVIT 300
Qy 301 ILYISLGLGLYQFGANIQSGITLNLPCWLYQSVKLLYSIGIFTYALQFVVAEIIIP 360
Db 301 ILYISLGLGLYQFGANIQSGITLNLPCWLYQSVKLLYSIGIFTYALQFVVAEIIIP 360
Qy 361 FFVSRAPHECHLAVDLFVRTVLVCITLAILIPRLDLVILSGVSSSALALIIPPLE 420
Db 361 VIVSWCKCTLMVDLIGSAMLCKTCLAILIPRLDLVILSGVSSSALALIIPPLE 420

Qy 421 VTFYSEGMSPLTIFKDALISILGVGVGVGTVEALYELIQPSNAPIFINSTCAFI 476
Db 421 VTFYSEGMSPLTIFKDALISILGVGVGVGTVEALYELIQPSNAPIFINSTCAFI 476
RESULT 9
ADF90169
ID ADF90169 standard; protein; 476 AA.
AC ADF90169;
XX
DT 26-FEB-2004 (first entry)
DE Human transporter homologue seq id 7.
KW peptide therapy; transporter; human.
XX
OS Homo sapiens.
XX
XX US2003170778-A1.
XX
XX 11-SEP-2003.
XX
XX 14-MAR-2001; 2001US-00805456.
XX
XX 22-DEC-2000; 2000US-0257175P.
XX
XX (WEIM/) WEI M.
XX (YANC/) YAN C.
XX (MERC/) MERKLOV G V.
XX (KERC/) KETCHUM K A.
XX (DFRA/) DI FRANCESCO V.
XX (BEAS/) BEASLEY E M.
XX
XX Wei M, Yan C, Merklov GV, Ketchum KA, Di Francesco V, Beasley EM;
XX WPI; 2003-898259/82.
XX
XX New human transporter peptide, useful for preparing a composition for
XX treating a disease or condition mediated by human transporters.
XX
XX Disclosure; SEQ ID NO 7; 94pp; English.
XX
XX The invention describes an isolated peptide comprising a 476 amino acid
XX sequence (S1) or its allelic variant, orthologue or fragment, where the
XX allelic variant or orthologue is encoded by a nucleic acid that
XX hybridises under stringent conditions to the opposite strand of a nucleic
XX acid comprising a sequence having 2093 or 46649 base pairs, and the
XX fragment comprises 10 contiguous amino acids of S1. The peptide is useful
XX for preparing a composition for treating a disease or condition mediated
XX by a human transporter protein. This is the amino acid sequence of a
XX human transporter protein homologue.
XX
XX Sequence 476 AA;
SQ
Query Match 94.1%; Score 2324; DB 7; Length 476;
Best Local Similarity 94.5%; Pred. No. 3.8e-242;
Matches 450; Conservative 9; Mismatches 17; Indels 0; Gaps 0;
Qy 1 MSTQRLNEDYHDSSTDVSPSESGLNLSPPSGSYQRFQGSNTTWFQTLIHLKGN 60
Db 1 MSTQRLNEDYHDSSTDVSPSESGLNLSPPSGSYQRFQGSNTTWFQTLIHLKGN 60
Qy 61 IGTGLGLPLAVKAGIWMGPISLLIIGIVAVHGMGILVKAHFCRLNKSFDYDGTIV 120
Db 61 IGTGLGLPLAVKAGIWMGPISLLIIGIVAVHGMGILVKAHFCRLNKSFDYDGTIV 120
Qy 121 MYGLESPCSWLNRHAGRWVDFLLVITQFGCCVYFVLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSWLNRHAGRWVDFLLVITQFGCCVYFVLADNFKQVIEAANGTTNNC 180
Qy 181 HNNETVILPTMTDSRLYMLSPFLPLVLLVFIRNLRALSIFSLANITMLVSLVMYQFIV 240

Db	181	HNNETVLTPTMDSRLYMSFLPFLVLLVFIRNLRLSIFSLLANITMLVSLVMIYQFIV	240
Qy	241	QRIIPDPSHLPLVAPWKTYPLFFGTAIFSPFEGIGWVLPLENKMDPRKFPILYLGMVIVT	300
Db	241	QRIIPDPSHLPLVAPWKTYPLFFGTAIFSPFEGIGWVLPLENKMDPRKFPILYLGMVIVT	300
Qy	301	ILYISLGLCYLQFGANIQGSITLNLPCWLYQSVKLLYSIGIFFYFVALQFYVPAEIIIP	360
Db	301	ILYISLGLCYLQFGANIQGSITLNLPCWLYQSVKLLYSIGIFFYFVALQFYVPAEIIIP	360
Qy	361	FFVSRAPHECELVDLFFVRLVCLTCILAILPRDLVLSLVGSSSSALALIIPPLE	420
Db	361	VIVSWWCKCTLMVDLGIGSAMLCKTCILAILPRDLVLSLVGSSSSALALIIPPLE	420
Qy	421	VTFYSEGMSPLTIFKDALISILGFGVGVGTVEALYELIQSNAPIFINSTCAFI	476
Db	421	VTFYSEGMSPLTIFKDALISILGFGVGVGTVEALYELIQSNAPIFINSTCAFI	476
RESULT 10			
ADRO3804			
ID	ADRO3804	standard; protein; 476 AA.	
XX	AC	ADRO3804;	
XX	DT	21-OCT-2004 (first entry)	
XX	DE	Human homologue of novel transporter protein.	
XX	KW	Human; transporter.	
XX	OS	Homo sapiens.	
XX	PN	US2004146887-A1.	
XX	PD	29-JUL-2004.	
XX	PF	07-OCT-2003; 2003US-00679362.	
XX	PR	22-DEC-2000; 2000US-0257175P.	
XX	PR	14-MAR-2001; 2001US-00805456.	
XX	PA	(APPL-) APPLERA CORP.	
XX	PI	Wei M, Yan C, Merklov G, Ketchum KA, Difrancesco V, Beasley EM;	
XX	XX	WPI; 2004-552659/53.	
XX	PT	New nucleic acid encoding human transporter peptides, useful for	
XX	PT	preparing agents for treating a disease or condition mediated by human	
XX	PT	transporters.	
XX	PS	Disclosure; SEQ ID NO 7; 62pp; English.	
XX	CC	The invention relates to a new isolated nucleic acid comprising a	
XX	CC	sequence encoding a transporter protein (appearing as ADR03799) and	
XX	CC	appearing as ADR03798 (the cDNA) or ADR03800 (the gene). Also included	
XX	CC	are a vector comprising the isolated nucleic acid, a host cell containing	
XX	CC	the vector, producing the polypeptide, detecting the presence of the	
XX	CC	nucleic acid in a sample and an isolated human peptide having a sequence	
XX	CC	that shares at least 70% homology with ADR03799. The gene encoding the	
XX	CC	human transporter is located on chromosome 5. The peptide is useful for	
XX	CC	preparing agents for treating a disease or condition mediated by a human	
XX	CC	transporter protein. The present sequence represents a homologue of the	
XX	CC	transporter protein.	
XX	SQ	Sequence 476 AA;	
Query Match		94.1%; Score 2324; DB 8; Length 476;	
Best Local Similarity		94.5%; Pred. No. 3.8e-242;	
Matches 450; Conservative		9; Mismatches 17; Indels 0; Gaps 0;	

Qy	1	MSTQRLRNEDYDYSSTVSPRESPEGLNNLSSPCGYQRFQGSNSTTWFQTLIHLKGN	60
Db	1	MSTQRLRNEDYDYSSTVSPRESPEGLNNLSSPCGYQRFQGSNSTTWFQTLIHLKGN	60
Qy	61	IGTGLLGLPLAVKNAGIVMGPIISLLIIGIVAVHGMGILVKCAHFCRRLNKSFVDYGDIV	120
Db	61	IGTGLLGLPLAVKNAGIVMGPIISLLIIGIVAVHGMGILVKCAHFCRRLNKSFVDYGDIV	120
Qy	121	MYGLESSPCSWLRNHAHWGRVVDFFLI VTQLGFCVCYFVFLADNFKQVIEAANGTTNNC	180
Db	121	MYGLESSPCSWLRNHAHWGRVVDFFLI VTQLGFCVCYFVFLADNFKQVIEAANGTTNNC	180
Qy	181	HNNETVILPTWDSRLYMSFLPFLVLLVFIRNLRLSIFSLLANITMLVSLVMIYQFIV	240
Db	181	HNNETVILPTWDSRLYMSFLPFLVLLVFIRNLRLSIFSLLANITMLVSLVMIYQFIV	240
Qy	241	QRIIPDPSHLPLVAPWKTYPLFFGTAIFSPFEGIGWVLPLENKMDPRKFPILYLGMVIVT	300
Db	241	QRIIPDPSHLPLVAPWKTYPLFFGTAIFSPFEGIGWVLPLENKMDPRKFPILYLGMVIVT	300
Qy	301	ILYISLGLCYLQFGANIQGSITLNLPCWLYQSVKLLYSIGIFFYFVALQFYVPAEIIIP	360
Db	301	ILYISLGLCYLQFGANIQGSITLNLPCWLYQSVKLLYSIGIFFYFVALQFYVPAEIIIP	360
Qy	361	FFVSRAPHECELVDLFFVRLVCLTCILAILPRDLVLSLVGSSSSALALIIPPLE	420
Db	361	VIVSWWCKCTLMVDLGIGSAMLCKTCILAILPRDLVLSLVGSSSSALALIIPPLE	420
Qy	421	VTFYSEGMSPLTIFKDALISILGFGVGVGTVEALYELIQSNAPIFINSTCAFI	476
Db	421	VTFYSEGMSPLTIFKDALISILGFGVGVGTVEALYELIQSNAPIFINSTCAFI	476
RESULT 11			
ADAS5508			
ID	ADAS5508	standard; protein; 434 AA.	
XX	AC	ADAS5508;	
XX	DT	20-NOV-2003 (first entry)	
XX	DE	Human protein, SEQ ID 3076.	
XX	KW	Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;	
XX	KW	Gene Therapy; human; secretory protein; membrane proteins; cancer;	
XX	KW	inflammatory disease; osteoporosis; neurological disease.	
XX	OS	Homo sapiens.	
XX	PN	EP1293569-A2.	
XX	PD	19-MAR-2003.	
XX	PF	21-MAR-2002; 2002EP-00006586.	
XX	PR	14-SEP-2001; 2001JP-00328381.	
XX	PR	24-JAN-2002; 2002US-0350435P.	
XX	PA	(HELI-) HELIX RES INST.	
XX	PA	(REAS-) RES ASSOC BIOTECHNOLOGY.	
XX	PI	Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;	
XX	PI	Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Tamechika I;	
XX	PI	Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;	
XX	XX	WPI; 2003-395539/38.	
XX	DR	N-PSDB; ADA53869.	
XX	PT	New polynucleotides encoding full-length polypeptides, e.g. secretory	
XX	PT	and/or membrane proteins, useful for developing medicines for diseases in	
XX	PT	which the gene is involved, or as target molecules for gene therapy.	
XX	XX	Claim 14; SEQ ID NO 3076; 205pp; English.	


```
XX The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA5710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 434 AA;

Query Match      89.8%; Score 2217; DB 6; Length 434;
Best Local Similarity 90.8%; Pred. No. 1.3e-230;
Matches 432; Conservative 1; Mismatches 1; Indels 42; Gaps 1;

Qy 1 MSTQRLNEDYHDSSTDVSPSESPSEGLNLSFGSYQRFQGSNSTTWFQTLIHLKGN 60
Db 1 MSTQRLNEDYHDSSTDVSPSESPSEGLNLSFGSYQRFQGSNSTTWFQTLIHLKGN 60

Qy 61 IGTGLGLPLAVKAGIVMGPIISLLIIGIVAVHCHGILVKCAHFCRLNKSFDVYDGTV 120
Db 61 IGTGLGLPLAAKNAGIVMGPIISLLIIGIVAVHCHGILVKCAHFCRLNKSFDVYDGTV 120

Qy 121 MYGLESPCSWLNRNHAHGRVDFFLIVTQLGFCVYFVLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSWLNRNHAHGRVDFFLIVTQLGFCVYFVLADNFKQVIEAANGTTNNC 180

Qy 181 HNNETVILTPMTDSRLYMLSPFLPVLVLFIRNLRALSIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNNETVILTPMTDSRLYMLSPFLPVLVLFIRNLRALSIFSLLANITMLVSLVMIYQFIV 240

Qy 241 QRIPDPHPLVAPWKTYPLFFGTAFISFEGIGMWLPLENKMKDPRKPLIYLGMWIVT 300
Db 241 QRIPDPHPLVAPWKTYPLFFGTAFISFEGIGMWLPLENKMKDPRKPLIYLGMWIVT 300

Qy 301 ILYISLGLCYLQFGANIQGSITLNLPCNWLQSVKLLYSIGIFPTYALQFVPAEIIIP 360
Db 301 ILYISLGLCYLQFGANIQGSITLNLPCNWLQSVKLLYSIGIFPTYALQFVPAEIIIP 360

Qy 361 FFVSRAPHECHLVVDLFFVTVLVCITLAILPRDLVLSVSVSSSALALIIPPLLE 420
Db 361 FFVSRAPHECHLVVDLFFVTVLVCITLAILPRDLVLSVSVSSSALALIIPPLLE 420

Qy 421 VTFYSEGMSPLTIKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 476
Db 379 VTFYSEGMSPLTIKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 434

RESULT 12
ADSI1015
XX ADSI1015 standard; protein; 434 AA.
XX AC ADSI1015;
XX
XX 16-DEC-2004 (first entry)
XX Human therapeutic protein - SEQ ID 1252.
XX
XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnery;
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy.
XX
XX Homo sapiens.
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang Yt, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI
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PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX WPI; 2004-668857/65.
DR N-PSDB; ADS10331.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.
XX
XX Claim 20; SEQ ID NO 1252; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.
XX
SQ Sequence 434 AA;

Query Match      89.8%; Score 2217; DB 8; Length 434;
Best Local Similarity 90.8%; Pred. No. 1.3e-230;
Matches 432; Conservative 1; Mismatches 1; Indels 42; Gaps 1;

Qy 1 MSTQRLNEDYHDSSTDVSPSESPSEGLNLSFGSYQRFQGSNSTTWFQTLIHLKGN 60
Db 1 MSTQRLNEDYHDSSTDVSPSESPSEGLNLSFGSYQRFQGSNSTTWFQTLIHLKGN 60

Qy 61 IGTGLGLPLAVKAGIVMGPIISLLIIGIVAVHCHGILVKCAHFCRLNKSFDVYDGTV 120
Db 61 IGTGLGLPLAAKNAGIVMGPIISLLIIGIVAVHCHGILVKCAHFCRLNKSFDVYDGTV 120

Qy 121 MYGLESPCSWLNRNHAHGRVDFFLIVTQLGFCVYFVLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSWLNRNHAHGRVDFFLIVTQLGFCVYFVLADNFKQVIEAANGTTNNC 180

Qy 181 HNNETVILTPMTDSRLYMLSPFLPVLVLFIRNLRALSIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNNETVILTPMTDSRLYMLSPFLPVLVLFIRNLRALSIFSLLANITMLVSLVMIYQFIV 240

Qy 241 QRIPDPHPLVAPWKTYPLFFGTAFISFEGIGMWLPLENKMKDPRKPLIYLGMWIVT 300
Db 241 QRIPDPHPLVAPWKTYPLFFGTAFISFEGIGMWLPLENKMKDPRKPLIYLGMWIVT 300

Qy 301 ILYISLGLCYLQFGANIQGSITLNLPCNWLQSVKLLYSIGIFPTYALQFVPAEIIIP 360
Db 301 ILYISLGLCYLQFGANIQGSITLNLPCNWLQSVKLLYSIGIFPTYALQFVPAEIIIP 360

Qy 361 FFVSRAPHECHLVVDLFFVTVLVCITLAILPRDLVLSVSVSSSALALIIPPLLE 420
Db 361 FFVSRAPHECHLVVDLFFVTVLVCITLAILPRDLVLSVSVSSSALALIIPPLLE 420

Qy 421 VTFYSEGMSPLTIKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 476
Db 379 VTFYSEGMSPLTIKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 434

RESULT 13
ABP96446
XX ID ABP96446 standard; protein; 475 AA.
XX AC ABP96446;
XX
XX 02-JUN-2003 (first entry)
XX
XX Rat LYAAT-1 protein SEQ ID NO:41.
XX
XX Neuroprotective; nootropic; cerebroprotective; analgesic; gene therapy;
XX central nervous system disorder; CNS disorder; multiple sclerosis;
XX
```


QY 121 MYGLESSPCWLNHNAHGRYVDFFLIVTQIGFCVYFVFLADNFKQVIEAANGTTNNC 180
DB 120 MYGLECSPTWVRNHSWGRRIVDFFLIVTQIGFCVYFVFLADNFKQVIEAANGTTNC 179
QY 181 HNETVILPTMDSRLYMLSPFLVLVFIIRNLRLALSIFSLANITMLVSLVMIYQFIV 240
DB 180 NNVTVIPTPTMDSRLYMLSPFLVLVFIIRNLRLALSIFSLANITMLVSLVMIYQFIV 239
QY 241 QRIIDPDLPLVAPKTYPLFFGTAFIFEGIGVWLPLENKMDPKRPFLLIYLGMVIT 300
DB 240 QRIIDPDLPLVAPKTYPLFFGTAFIFEGIGVWLPLENKMDPKRPFLLIYLGMVIT 299
QY 301 ILYISLGLYQFQGANIQGSITLNLPCWLYQSVKLLYSIGIFTYALQFVPAEIIIP 360
DB 300 VLYISLGLYQFQGANIQGSITLNLPCWLYQSVKLLYSIGIFTYALQFVPAEIIIP 359
QY 361 FVSRAPHECHLVVDLFRVTVLVCLTCLAILIPRLDLVSLVGVSSSALALIIPPLE 420
DB 360 AIVSRVPEHFLVVDLFCVRTAMVCTCLAILIPRLDLVSLVGVSSSALALIIPPLE 419
QY 421 VTFYSEGMSPITTFKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 476
DB 420 VTTYGEGISPLTITKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 475

RESULT 15
ABB76935
ID ABB76935 standard; protein; 475 AA.
XX AC ABB76935;
XX DT 22-JUL-2002 (first entry)
XX DE Rat VG51.
XX KW Rat; antiaesthetic; anxiolytic; antiepileptic; antihypertensive;
KW psychotropic; glutamate transporter; transporter; GABA;
KW gamma-aminobutyric acid transporter; GABA transporter; neurotransmitter;
KW asthma; anxiety; epilepsy; hypertension; psychiatric disorder;
KW neurotic disorder; VG51.
XX OS Rattus sp.
XX PN WO200071709-A1.
XX PD 30-NOV-2000.
XX PF 19-MAY-2000; 2000WO-FR001383.
XX PR 21-MAY-1999; 99FR-00006525.
XX XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
XX PI Giros B, Gasnier B, Sagne C, El Mestikawy S, Hamon M;
XX WPI; 2001-025160/03.
XX DR N-PSDB; ABL57913.
XX PT New mammalian amino acid transporter, used e.g. to screen for
XX psychotropic agents, is high capacity but low affinity transporter of
XX gamma-aminobutyric acid.
XX FS Claim 2; Fig 2; 103pp; French.
XX CC The present sequence is the protein sequence for rat VG51, a glutamate/
CC gamma-aminobutyric acid (GABA) transporter. GABA and glutamate are
CC neurotransmitters. The transporter can be used to produce specific
CC antibodies, to screen for binding agents. Modulators of the transporter
CC are useful for treating disorders associated with deregulated
CC glutamate/GABA transport, e.g. asthma, anxiety, epilepsy, hypertension
CC and other psychiatric and neurotic disorders, while determining levels of
CC the transporter and its coding sequence can be used for diagnosis of such

CC disorders
XX SQ Sequence 475 AA;
Query Match 86.8%; Score 2142.5; DB 4; Length 475;
Best Local Similarity 85.5%; Pred. No. 1.7e-222;
Matches 407; Conservative 37; Mismatches 31; Indels 1; Gaps 1;
QY 1 MSTQRLRNEDYHDSSTDVSPSESEGLNNLSPSGYQRFQSNSTTWFTQLIHLKGN 60
DB 1 MSTQRLRNEDYHDSSTDVSPSESEGLNSP-SPGSYQRLGENSMTWFTQLIHLKGN 59
QY 61 IGTGLLGLPLAVKAGIVMGPIISLIIIGIVAVHMGILVKCAHFCRRLNKSFVDYDVT 120
DB 60 IGTGLLGLPLAVKAGILGLPLSLIIGIVAVHMGILVKCAHFCRRLNKSFVDYDVT 119
QY 121 MYGLESSPCWLNHNAHGRYVDFFLIVTQIGFCVYFVFLADNFKQVIEAANGTTNNC 180
DB 120 MYGLECSPTWVRNHSWGRRIVDFFLIVTQIGFCVYFVFLADNFKQVIEAANGTTNC 179
QY 181 HNETVILPTMDSRLYMLSPFLVLVFIIRNLRLALSIFSLANITMLVSLVMIYQFIV 240
DB 180 NNVTVIPTPTMDSRLYMLSPFLVLVFIIRNLRLALSIFSLANITMLVSLVMIYQFIV 239
QY 241 QRIIDPDLPLVAPKTYPLFFGTAFIFEGIGVWLPLENKMDPKRPFLLIYLGMVIT 300
DB 240 QRIIDPDLPLVAPKTYPLFFGTAFIFEGIGVWLPLENKMDPKRPFLLIYLGMVIT 299
QY 301 ILYISLGLYQFQGANIQGSITLNLPCWLYQSVKLLYSIGIFTYALQFVPAEIIIP 360
DB 300 VLYISLGLYQFQGANIQGSITLNLPCWLYQSVKLLYSIGIFTYALQFVPAEIIIP 359
QY 361 FVSRAPHECHLVVDLFRVTVLVCLTCLAILIPRLDLVSLVGVSSSALALIIPPLE 420
DB 360 AIVSRVPEHFLVVDLFCVRTAMVCTCLAILIPRLDLVSLVGVSSSALALIIPPLE 419
QY 421 VTFYSEGMSPITTFKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 476
DB 420 VTTYGEGISPLTITKDALISILGFVGVGTYEALYELIOPSNAPIFINSTCAFI 475

Search completed: August 24, 2006, 01:19:44
Job time : 196 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 24, 2006, 01:19:59 ; Search time 41 Seconds
(without alignments)
1117.053 Million cell updates/sec

Title: US-10-679-362-2

Perfect score: 2469

Sequence: 1 MSTQRLRNEDYHYSSTDVS.....YELIQSNAPIFINSTCAFI 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1677.5	67.9	481	2 JC7961	proton-coupled ami
2	672	27.2	607	2 T26845	hypothetical prote
3	652	26.4	449	2 H80022	protein T27A1.5 [i
-4	465.5	18.9	436	2 T05653	amino acid transpo
5	465.5	18.9	713	2 S58251	probable membrane
6	464	18.8	434	2 T15799	hypothetical prote
7	462.5	18.7	481	2 T23131	hypothetical prote
8	443.5	18.0	460	2 F88544	protein F59B2.2 [i
9	431.5	17.5	467	2 T26705	hypothetical prote
10	415	16.8	656	2 T38741	major facilitator
11	388.5	15.7	692	2 S37976	hypothetical prote
12	368	14.9	389	2 S31123	hypothetical prote
13	285.5	11.6	543	2 T48239	hypothetical prote
14	276	11.2	516	2 T48238	hypothetical prote
15	274.5	11.1	426	2 T51506	hypothetical prote
16	270.5	11.0	529	2 E84813	hypothetical prote
17	263	10.7	503	2 T26524	hypothetical prote
18	259	10.5	890	2 T21000	hypothetical prote
19	251.5	10.2	462	2 S42372	hypothetical prote
20	251.5	10.2	486	2 T42254	amino acid permeas
21	247	10.0	423	2 T49959	hypothetical prote
22	233.5	9.5	571	2 T06737	hypothetical prote
23	233	9.4	484	2 T34016	hypothetical prote
24	232	9.4	509	2 S45413	probable membrane
25	230	9.3	494	2 T16658	hypothetical prote
26	224	9.1	476	2 C96505	probable amino aci
27	222	9.0	505	2 B88206	protein F21D12.3 [
28	215.5	8.7	485	2 A48187	amino acid transpo
29	210	8.5	448	2 S50622	hypothetical prote

ALIGNMENTS

RESULT 1

JC7961

proton-coupled amino acid transporter 2 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003

C:Accession: JC7961

R:Chen, Z.; Kennedy, D.J.; Wake, K.A.; Zhuang, L.; Ganapathy, V.; Thwaites, D.T.

Biochem. Biophys. Res. Commun. 304, 747-754, 2003

A:Title: Structure, tissue expression pattern, and function of the amino acid transporter

A:Reference number: JC7961; PMID:12727219

A:Accession: JC7961

A:Molecule type: mRNA

A:Residues: 1-481 <CH>

A:Experimental source: (Lung)

C:Comment: This transport protein is a second member of H⁺-coupled, pH-dependent, Na⁺-in-

sport not only from one cellular compartment to another (across plasma membranes) but al

C:Genetics:

A:Gene: pat2

A:Map position: 10q22

C:keywords: amino acid transport system; PAT2

Query Match	67.9%	Score	1677.5	DB 2	Length	481			
Best Local Similarity	71.7%	Pred. No.	2.7e-127						
Matches	325	Conservative	54	Mismatches	67	Indels	7	Gaps	1
QY	20	SPESPSEGLNLSPPGSYQRFQGSNSTTWFOTLIHLKGNIGTGLLGLPLAVKNAGIVM	79						
Db	32	SQDPNPVNGSSSESE-----KTKGKITGFQTLVHLVKGNGGTGILGLPLAVKNAGILM	84						
QY	80	GPISLLIIGIVAVHGMGLVKCAHFCRLNKSFDYGDVTVMYGLSESPCSWLRNHAHWG	139						
Db	85	GPLSLLVWGLIACHMHLVRCARQFCHRLNKPMDYGDVTVMHGLASSPNTWLOSHAHWG	144						
QY	140	RRVDFELIVTLQGFCCVYFVFLADNFQVIEAANGTNNCHNETVILTPMDSRLYML	199						
Db	145	RHAVSFELIVTLQGFCCVYFVFLADNLKQVVEAVNSTTISCHKNETVILTPIDSLRYML	204						
QY	200	SFLPFLVLLVIRNLRALSIFSLANITMVLVSLVMYQFIVQRIQIPDPHPLVAPWKYTP	259						
Db	205	AFLPVGLLVIRNLRVLTIFSLANVSLVSLVIQGIQIPDPSPQLPVASWKYTP	264						
QY	260	LFPGTAFSPEGIMVLPLENKMDPKRFPILLVGMVITVLTLSLCLGVLQFGANIQ	319						
Db	265	LFPGTAFSPESIGVVLPLENKMDARRFPITLSLGMISITITLYIAIGALGLVREGDDIK	324						
QY	320	GSITINLPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFVSVRAPEHCELVVDLFR	379						
Db	325	ASITINLPNCWLYQSVKLLYVVGILCTHALQFYVPAEIIIPVASQVSKRWALPVDLSIR	384						
QY	380	TVLVCLTCILAILPRDLVLSVGSVSSSALALIIPPLLEVTVTYSGMGLPTTFKQAL	439						
Db	385	LALVCVTCMLAILPRDLVLSVGSVSSSALALIIPPLLEVTVTYGEGMSPLTTKQAL	444						

Db 37 FKTFAVFIYVAGVGLGLPYAFKRTGMLGVLLSVSVLTHRCMLLV-----YTRRK 91
Qy 110 NKSE-----VDYGDVTVMYGLSSPCSWLRNHAHWRVVDFFLIVTQLGFCVCYFVFL 162
Db 92 LDSFNAGISKIGSGD-----LGFVCGSL-----GRIVVDLFIILSQAGFCVGLIFI 140
Qy 163 ADNPKQVIEAANGTT--NNCHNETVILTP-----MDSRLYMLSFPLPF 205
Db 141 -----GTTLANLSDPE-----SPTSLRHQFTRLGSEFLGVSSKSLIYIWGCFPFQ 184
Qy 206 VLLVFIRNLRLSIFSLLANI-----TMLSVLMIYQFIVQRI-PDPShLPLVAPKTYPLF 261
Db 185 LGLNSIKTLTHLAPLSIFADIVDLCAMAVIVDESMLILKORPD-----VVAEGGMSLF 238
Qy 262 ---PGTAIFSPGEGIMVPLENKMDPKFPLIILYLGWIVITILYISLGLCYGLYQFGANI 318
Db 239 LYGNVAVYSEGVGVVPLESEMCKDKFKGVLAGNGFISLIYIARGLILGLAFGEDT 298
Qy 319 QGSTITLNPCLWYOSVKLYSIGIFFTYALQFVVPABIIIPFFVSRAPHECELVDLFLV 378
Db 299 MDIITANLGLAVSTVVLQGLCINLFTFTPLMNPVFEIVERRF--SRG-----MYSAWL 351
Qy 379 RTVLVCLTCLAILPRLDLVLISLVGSSSALALIPPLLEVTFYSEGMSPLTIKOA 438
Db 352 RWLLVLAVTLVALFVNPADFSLVSGSTCCVGLGVLPALPHLLVF--KEEMGLQWSSDT 410
Qy 439 LISILGFVGVVGYEALYEL 459
Db 411 AIVLVGVVLAAGTWSLSEI 431

RESULT 5
S58251
Probable membrane protein YNL101w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N2185
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1996 #sequence revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: S58251; S63041; S63953
R;Saiz, J.E.; Buitrago, M.J.; Soler, A.; del Rey, F.; Revuelta, J.L.
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of a 21.3 kb fragment from the left arm of yeast chromosome
A;Reference number: S58246
A;Accession: S58251
A;Molecule type: DNA
A;Residues: 1-713 <SAI>
A;Cross-references: UNIPROT:P50944; UNIPARC:UPI000005256D; EMBL:Z50161; NID:g929846; PID
R;Saiz, J.E.; Buitrago, M.J.; Soler-Mira, A.; del Rey, F.; Revuelta, J.L.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63037
A;Accession: S63041
A;Molecule type: DNA
A;Residues: 1-713 <SAW>
A;Cross-references: UNIPARC:UPI000005256D; EMBL:Z71377; NID:gl302013; PIDN:CAA95977.1; F
A;Experimental source: strain S288C
R;Saiz, J.E.; Buitrago, M.J.; Soler-Mira, A.; del Rey, F.; Revuelta, J.L.
Yeast 12, 403-409, 1996
A;Title: The sequence of a 21.3 kb DNA fragment from the left arm of yeast chromosome XI
A;Reference number: S63948; MUID:96267765; PMID:8701612
A;Accession: S63953
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-713 <SAF>
A;Cross-references: UNIPARC:UPI000005256D; EMBL:Z50161; NID:g929846; PIDN:CAA90525.1; PI
C;Genetics:
A;Cross-references: SGD:S0005045
A;Map position: 14L
A;Note: YNL101w
C;Superfamily: Saccharomyces cerevisiae probable membrane protein YNL101w
C;Keywords: transmembrane protein
F;302-318/Domain: transmembrane #status predicted <TM1>
F;374-390/Domain: transmembrane #status predicted <TM2>
F;410-426/Domain: transmembrane #status predicted <TM3>
F;442-458/Domain: transmembrane #status predicted <TM4>

F;486-502/Domain: transmembrane #status predicted <TM5>
F;516-532/Domain: transmembrane #status predicted <TM6>
F;557-573/Domain: transmembrane #status predicted <TM7>
F;626-642/Domain: transmembrane #status predicted <TM8>
F;649-665/Domain: transmembrane #status predicted <TM9>
F;689-705/Domain: transmembrane #status predicted <TM10>

Query Match 18.9%; Score 465.5; DB 2; Length 713;
Best Local Similarity 31.0%; Pred. No. 1.3e-29;
Matches 144; Conservative 81; Mismatches 167; Indels 73; Gaps 18;

Qy 32 LSSPGSVQRQCSNST--WFQTLHLKNGINTGTLGLPLAVKNAGIVMGFISLLIIGIV 90
Db 281 LSRPDHMKVLPSAKGTSTTKKVFILKSPFISGTVLFPNAPHNGGLFFSVSMIAFFGIY 340
Qy 91 AVHCGMGLVLCVCAHFCRRLNKSFDYDGTVMYGLSSPCSWLRNHAHWRVVDFFLIVT 150
Db 341 SYWCYYILVQ--AKSSCG--VSSFGDIG-----LKLPGPMRIILFSLVIT 383
Qy 151 QLGFCCVYFVLADNFQKQVIEAANGTTNNCHNETVILTPMDSRLYMLSFPLVL--LV 209
Db 384 QVGFSGAYMIPTAKNLQAFLD-----NVFH-----VGLPLS-----YLMVFQTIIFILS 429
Qy 210 FIRNLRLSIFSLLANITMLSVLMIYQFIVQRI-PDPShLPLVA-----PWKTYPL 260
Db 430 FIRNISKLSPSLANFFIMAGLVIVIIFTAKRLFFDLMGTPAMGVVGLNADRW---TL 486
Qy 261 PFGTAFSPGEGIMVPLENKMDPKFPLIILYLGWIVITILYISLGLCYGLQFQGANIQG 320
Db 487 FIGTAIFAFEGIGLIIPVQDSMRNPEKFLVALVILTATILFISIALTGLAYGSNVQT 546
Qy 321 SITLNPCLWYOS--VKLYSIGIFFTYALQFVVPABIIIPFFVSRAPHECELV-- 373
Db 547 VILLNLQSNIFVNLIOLFYSIAIMLSPTLQFPAIKIENKFFPKFKIYVGHDDLTR 606
Qy 374 VDL-----FVRTVLVCLTCLAIL--IPRLDIVLSLVCSSSALALIIIP 416
Db 607 VELRPNSGKLNWKIKLKNFIRSIIVVSIAYFGSDNLDKFKVSVIGSLACIPLVVIYP 666
Qy 417 PLLRVT--TFYSEGMSPLTIKDALISILGVFGV---FVVGTYEALY 457
Db 667 SMLHLRGNLSPETKGEFWRFAKPLMDTILIFGSIASMLYTSQSIF 711

RESULT 6
T15799
hypothetical protein C4487.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15799
R;Du, Z.
submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid C4487.
A;Reference number: S61146
A;Accession: T15799
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-434 <DUZ>
A;Cross-references: UNIPROT:Q18595; UNIPARC:UPI000017B834; EMBL:U28928; NID:g861301; PID
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:C44B7.6
A;Introns: 22/2; 52/3; 82/2; 113/2; 141/3; 196/3; 250/1; 293/2; 356/1

Query Match 18.8%; Score 464; DB 2; Length 434;
Best Local Similarity 30.1%; Pred. No. 1e-29;
Matches 125; Conservative 85; Mismatches 177; Indels 28; Gaps 9;

Qy 53 LIHLKNGIGTGLGLPLAVKNAGIVMGFISLLIIGIVAVHVCMLVKCAHHFCRRLNKS 112
Db 27 LINLMKMLGAGCSFSPAFKQSGVSLVILVIGLFCALCMILKLVKAGYLSKVNSA 86
Qy 113 FVDYGDVTVMYGLSSPCSWLRNHAHWRVVDFFLIVTQLGFCVCYFVFLADNFKQVIEA 172

Db 87 PLYDGN-MAYKATQASYPTRKAPVSRALVNSLCTILQIGCCCFYFVYVHLHELLEF 145
QY 173 ANGTNNCHNETVILPTWDSRLYMLSLPFLVLLVFIIRNLRAISFISLLANITMLVSL 232
Db 146 ---VMNDVPSRAT--LFPVW-----LPAFILLVSLSSMRALSIVSLGSGFLMLIAL 191
QY 233 -VMYQFIVQRI PDPHSLPILVAPMKTYPPLFFGTAIFSFEIGMVLPLENKMDPR--KFP 289
Db 192 AVIMFOLLTTEHKKLADLPVTDLMGIVSAAGTILVALEGOAMVLPLENRMKPKEDMKGP 251
QY 290 L-TLYLGMVITVILYISLGLCYLOFGANTQGSITLNPNCWLYQSOKLYSIFFTYA 348
Db 252 FGVLSVGMVGMVVIYSFAGFGLTYGNDVQDSITLNPNDHLGIFVKVALLFVYVSGFL 311
QY 349 LQFVPAEIIIPFVSRAPEHC-----ELVVDLFVRTLVLVCLTCLAILIPRLDIVSL 402
Db 312 IQVFPPIVAMIPAKKKLRTTCGVSTTKRIIVHFAFRYSIVIVVFLSYAIPRLSDMVPL 371
QY 403 VGVSSSALALIIPPLLEVTTFYSEGMSPLTIFKDALISILGFVGVVGYTYEALY 457
Db 372 VGVTAGMLLALVPSLPHLLILFQPCECRIGFLFDI---FLDFVCIILGMFFVIY 423
RESULT 7
T23131
hypothetical protein H32K16.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T23131
R;Wallis, J.
submitted to the EMBL Data Library, June 1997
A/Reference number: Z19691
A/Accession: T23131
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-481 <WIL>
A/Cross-references: UNIPROT:O62286; UNIPARC:UPI000007809E; EMBL:Z97191; PIDN:CAE10025.1;
A/Experimental source: clone H32K16
C/Genetics:
A/Gene: CESP:H32K16.1
A/Map position: 1
A/Introns: 64/2; 94/3; 124/2; 155/2; 183/3; 240/3; 337/2; 397/1; 444/2
C/Superfamily: Arabidopsis amino acid transport protein I
Query Match 18.7%; Score 462.5; DB 2; Length 481;
Best Local Similarity 28.7%; Pred. No. 1.5e-29;
Matches 123; Conservative 91; Mismatches 174; Indels 41; Gaps 8;
QY 53 LIHLKGNIGTGLGLPLAVKNAGIVMGPISSLIIIGIVAVHCMGILVKCAHFCRRLNKS 112
Db 69 LINFICWIGGCFSLAVSFQAGLWGLALVFIVGFLSLYSMHKIVNCQYLAKSNGDQ 128
QY 113 FVDYGDVTWYGLSSPCSWLRNHAHWGRRVDFLIVTQLGFCVCYVFLADNPKQVIEA 172
Db 129 SLDYGENAEAAQMS--YKWARHGKGLAKIVINACLLAFQLGVIITVFMVFAVEHVIEWEF 187
QY 173 ANGTNNCHNETVILPTWDSRLYMLSLPFLVLLVFIIRNLRAISFISLLANITMLVSL 232
Db 188 FADSP-----PPFSKCVMLMYFVP-QMLNFIIGHMKLLITLCLFGNVIIFAAI 235
QY 233 VMIYQFIVQRI PDPHSLPILVAPMKTYPPLFFGTAIFSFEIGMVLPLENKMDPRKF-- 288
Db 236 VLITKELMVHTWYPTWELGVSVTGIEGSLAAGALYSFEGQAMVLPWENSLKYPKDMTGA 295
QY 289 PLIILYGMVITVILYISLGLCYLOFGANTQGSITLNPNCWLYQSOKLYSIFFTYA 348
Db 296 TGVLTAMNLVTLVLYAFYFGFYVTFGPAVGQGSITLNPNSILTVSIRKGLVLKIFGSA 355
QY 349 LQFVPAEIIIPFVSRAPEHCCELVDLF---VRTLVLVCLTCLAILIPRLDIVSLVGS 405
Db 356 IQLYVIVQMLLPSLRKSIDEDKRVHRLPLPVALRLGLMLISLCTALIVPMLQIPLVGI 415

QY 406 VSSSALALIIPPLLEVTTFYSEGMSPLTIFK-----DALISILGFVGVWVG 451
Db 416 TSGLLISLILPSFLDCMVF-----LPVFKQOGDMFKFYQKLIINVLFLVGLWGFLLGAG 468
QY 452 TYEALYELI 460
Db 469 LYSSIDII 477
RESULT 8
F88544
protein F59B2.2 [imported] - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: F88544
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A/Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A/Reference number: A75000; MUID:99069613; PMID:9851916
A/Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A/Accession: F88544
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-460 <STO>
A/Cross-references: UNIPROT:P34479; UNIPARC:UPI000013B9DA; GB:chr_III; PIDN:CAA77582.1;
C/Genetics:
A/Gene: F59B2.2
A/Map position: 3
Query Match 18.0%; Score 443.5; DB 2; Length 460;
Best Local Similarity 26.7%; Pred. No. 4.7e-28;
Matches 128; Conservative 101; Mismatches 211; Indels 39; Gaps 10;
QY 6 LRNEDYDYSSTDVSPESPSEGLNMLSSPGSYORFGQSNSTTWFTOTLIHLKGNIGTGL 65
Db 1 MSEEGERARVTEGDAESMNDGRALVOPDA---RSGDVITPT--RAVLTLSKSMFNAGC 55
QY 66 LGULPLAVKNAGIVMGPISSLIIIGIVAVHCMGILVKCAHFCRRLNKSFDYDGTVMYGLE 125
Db 56 FSLPYAWKGLGLWVSFVMSFVIAGLWYGNHILVRASQHLAKKSDRSALDYGHFAKKVCD 115
QY 126 SSPCSWLNRHAHWGRRVDFLIVT---QLGECVYFVFLADNPKQVIEAANGTTNNCH 181
Db 116 YSDIRFLRNNSS---KAVMYFVNVTILFYOLGCVSAILFISDNLVNLVGDHLGGT--- 167
QY 182 NNETVILPTMDSRLYMLSLPFLVLLVFIIRNLRAISFISLLANITMLVSLVMIYQFIVQ 241
Db 168 RHQOMILMATVS-----LFFILLTNMFTEMRIVSFFALVSVFVIGAAVIMQYTVQ 219
QY 242 RIPDPHSLPILVAPMKTYPPLFFGTAIFSFEIGMVLPLENKMDPRKF--PL-ILYLGWVI 298
Db 220 QPNQWKLPAANTFTGTTIMGMSYAFEGQTMILPIENKLDNPAALAPFGVLSTTMII 279
QY 299 VTILYISLGLCYLOFGANTQGSITLNPNCWLYQSOKLYSIFFTYAQFVVPABII 358
Db 280 CTAFMTALGFYGTGFGDSIAPTITTNVPKEGLYSTVNVFLMQSLGNSIAMYVVYDMF 339
QY 359 I----PFFVSRAPHECELVDLFVRTLVLVCLTCLAILIPRLDIVSLVGSVSSSALALI 414
Db 340 FNGFRKRGARFNNVPKWLSDKGRFVFWLVLMVAVLIPKLEIMIPLVGTSGALCALI 399
QY 415 IPLLLEVTTFYSEGMSPLT-----IFKDALISILGFVGVVGYTYEALYELIQPSNAP 466
Db 400 FPPFFEMITFTWDKGLLTYRQMTKIFINLVWMAIGVFAIAGVYTNIIHAIIQSFSP 458
RESULT 9
T26705
hypothetical protein Y38H6C.17 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T26705

A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-132 <VA3>
A;Cross-references: UNIPARC:UPI0000168BC6; EMBL:Z26877; NID:g407482; PIDN:CAA81508.1; PI
A;Experimental source: strain S288C
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993
C;Genetics:
A;Cross-references: SGD:S0001629
A;Map position: 11L
A;Supfamily: Saccharomyces cerevisiae probable membrane protein YNL101W
C;Keywords: transmembrane protein

Query Match 15.7%; Score 388.5; DB 2; Length 692;
Best Local Similarity 28.9%; Pred. No. 1.9e-23;
Matches 131; Conservative 76; Mismatches 193; Indels 53; Gaps 14;

QY 8 NEDYHVSSTDVSPSPSGNLNLSPPGVSQVQFGQSNSTTQTLLHLKGNIGTGLIG 67
Db SEBEEBEEETEEPEEALTESTQLVSRHGRPHKSSV--KAVLLLKSFVGTGLVF 317
QY 68 LPLAVKNAGIVMGPIISLLIIGIVAVHCHGILVKCAHHFCRRLNKSFYD-YGD--TWMYGL 124
Db LPKAFHNGGWGFSALCLLSCALISYGCFSVLIITK-----DKVGVDGYGDMGRILYGP 370
QY 125 ESSPCSWLNRNHAHWRVDFLLIVTQLGCCVYFVPLADNFQVIEAANGTTNNCHNE 184
Db 371 KM-----KPAILLSALSQIGFSAAYTFVTATNLQVFS-----NFFH--- 408
QY 185 TVILTP-TMDSRLYMLSFLLVLLVFIIRLALSIFSLANTIMLVSLVMYQVQVRI 243
Db 409 ---LKPGSISLATYFAQVILFVPLSUTRNIAKLSGTALADUFLIGLVYTVYVSIYI 465
QY 244 -----PDPSHLPLVAPWKTYPFFGTAIFSEFEGIMVLPLENKMKDPKRPFLILYLMV 297
Db 466 AVNGVASDTMLMFKADWS---LFIGTAIFTEGIGLLIPIQESMKHPKHFPSLSAVMC 522
QY 298 IVTLTYTSLGCLGVLQFGANIQGSITNLNLCMWYQ-SVKLLYSIGIFFTYALQFYVPAE 356
Db 523 IVAVIFISGCLLCVAAGSDVKTVLLENFPODTSYTLTVQLLYALAILLSTPLQLFPAIR 582
QY 357 IITPF-FVSRAPHECELVDL---FVRTVLVCLTCILA-LIPLDLVISVGSVSSAL 411
Db 583 ILENWTFPSNAGSKYNPKVKNYFCAIVLVLSILAWGVANDLDRKFSVLVGSFACIPL 642
QY 412 ALIIPPLEVTFYFSEGSPLTFKDALISITL 444
Db 643 IYIYPLHLKASILSGTSRARLLLDLIVIVFG 675

RESULT 12
S31123
hypothetical protein F59B2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S31123
R;Sulston, J.; Du, Z.; Thomas, K.; Willson, R.; Hillier, L.; Staden, R.; Halloran, N.; G
awkins, T.; Ainscough, R.; Waterston, R.
submitted to the EMBL Data Library, November 1991
A;Description: The C. elegans sequencing project: A beginning.
A;Reference number: S31122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <SUL>
A;Cross-references: UNIPROT:P34479; UNIPARC:UPI000017BA50; EMBL:Z11505; NID:g6718; PID:g
A;Introns: 38/2; 59/2; 148/2; 343/3

Query Match 14.9%; Score 368; DB 2; Length 389;
Best Local Similarity 28.5%; Pred. No. 4.7e-22;
Matches 97; Conservative 72; Mismatches 141; Indels 30; Gaps 7;

QY 145 FFLIVT---QLGFCVYFVPLADNFQVIEAANGTTNNCHNETVILTPMTDSRLYMLS 200

Db 60 YFNVNITLQMGCSVALFISDNLVNLVGDHLGCT---RHQMLMATVS----- 108
QY 201 FLPLVLLVFIIRLALSIFSLANTIMLVSLVMYQVQVIRIPDPSPHLPVAPWKTYPL 260
Db 109 -LPFILLTNMFTMRIVSFVFFALVSSVFFVIGAAVIMQYTVQPNQWDKLPAPATNFTGIT 167
QY 261 FPGTALFSEFEGIMVLPLENKMKDPKRF--PL-ILYLGWIVITILYISLGLCYLQFGAN 317
Db 168 MIGMSYAFEGQTMILPIENKLDNPAFLAPFGVLSTTMIICTAFTAFWTALGFGYTGFGDS 227
QY 318 IQGSITLNLPCNWLQYOSVKLLYSIGIFFTVALQFYVPAEIII---PFFVSRAPHECHELV 373
Db 228 IAPTITNVPKCELYSTNVFLMLQSLGNSIAMVYVDMFFNGFRKFGARPNVPKWL 287
QY 374 VDLFVRTVLVCLTCILAIIPLRLDLVISVGSVSSALALIIPLPLEVTFYFSEGSPLT 433
Db 288 SDKGFVFWVLYTLMMAVLIPLKLEIMPLVGVTSALCALIFPPFFEMITFTWDKGLLT 347
QY 434 -----IFKDALISILGFVGVVGYEALYELIQPSNAP 466
Db 348 YRQRMTKIFINLVMAIGVFAIAGVYTNHAIQSFQSP 387

RESULT 13
T48239
hypothetical protein T7H20.230 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48239
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24488
A;Accession: T48239
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-543 <BEV>
A;Cross-references: UNIPROT:Q9LZL4; UNIPARC:UPI00000A3EP5; EMBL:AL162508
A;Experimental source: cultivar Columbia; BAC clone T7H20
C;Genetics:
A;Map position: 5
A;Introns: 74/2; 168/1; 234/1; 242/1; 302/1; 375/2; 420/3; 476/1; 490/3; 511/3
A;Note: T7H20.230
C;Superfamily: Arabidopsis amino acid transport protein I

Query Match 11.6%; Score 285.5; DB 2; Length 543;
Best Local Similarity 25.3%; Pred. No. 2.9e-15;
Matches 123; Conservative 85; Mismatches 183; Indels 95; Gaps 21;

QY 2 STORLNRDHYDYSST--DVSPEESPSEGNLNLSSPGSYQRFQGSNTTTFQTLIHLKLG 59
Db 119 SSKPILLSQPVDPKXETILPWNQSLKLSVTDLPLP-----EPNLCSPFSQSVLNTV 171
QY 60 NIGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHCHGILVKCAHHFCRRLNKS-----FV 114
Db 172 LCGLGLITMPYALIKESGWLGLPI-LLFVGVITCY-TGVLMK-----RLESSEGIOTYP 223
QY 115 DYGDVTVMYGLESPSPCSWLNRNHAHWRVDFLLIVTQLGCCVYFVPLADN---FKQV- 169
Db 224 DIQAA-FGITDSI-----RGVVP-----CVEIIMNSDLNLSGLFPNVS 262
QY 170 IEAANGTTNNCHNETVILTPMTDSRLYMLSFLLVLLVFIIRLALSIFS---LLANI 226
Db 263 LSIASGIS-----LDSFQIFAILTTLVLPL---TWMLKDLSSLVSLVSGVGLASI 309
QY 227 TMLVSLVMYQ-----FIVQRPDPSHLPVAPWKTYPLFFGTAFISFEGIGMVLPLEN 280
Db 310 LLGICLFWAGVDGIGFPHATGRVFDLSNLPT-----IGIFGFGSHSVFPNIYS 360
QY 281 KMKDPKRPFLILYLGWIVITILYISLGLCYLQFGANIQGSITNLNPNCLYQSVKLLYS 340
Db 361 SMKDPSPFPLVLVICSFCTVLIIAVACGYTFMGEAVESQFTLNMKPHFPFSPKVAWTA 420

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OM protein - protein search, using sw model

Run on: August 24, 2006, 01:16:39 ; Search time 303 Seconds
(without alignments)
1453.160 Million cell updates/sec

Title: US-10-679-362-2
Perfect score: 2469
Sequence: 1 MSTQRLRNEDYHDSSTVDS.....YELIQSNAPIFINSTCAFI 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_7.2:**

1: uniprot_sprot:**

2: uniprot_trembl:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2469	100.0	476	1 S36A1_HUMAN	Q722h8 homo sapien
2	2439	98.8	476	2 Q47m7_MACFA	Q47m7 macaca fasc
3	2317.5	93.9	475	2 Q2VPS4_RABIT	Q2VPS4 oryctolagus
4	2146.5	86.9	475	1 S36A1_RAT	Q924a5 rattus norv
5	2141.5	86.7	475	1 S36A1_MOUSE	Q84d3 mus musculus
6	2141.5	86.7	475	2 Q5F227_MOUSE	Q5F227 mus musculus
7	1722.5	69.8	483	2 Q495M3_HUMAN	Q495m3 homo sapien
8	1713.5	69.4	483	2 Q6ZWK5_HUMAN	Q6ZWK5 homo sapien
9	1711.5	69.3	483	2 Q726B5_HUMAN	Q726b5 homo sapien
10	1699.5	68.8	478	2 Q8BHK3_MOUSE	Q8bhk3 m adult mal
11	1696.5	68.7	478	2 Q8JZP1_MOUSE	Q8jzpl mus musculus
12	1689.5	68.4	479	2 Q6NRA6_XENLA	Q6nra6 xenopus lae
13	1677.5	67.9	481	2 Q8K415_RAT	Q8k415 rattus norv
14	1592	64.5	313	2 Q86YK4_HUMAN	Q86yk4 homo sapien
15	1476.5	59.8	470	2 Q726B4_HUMAN	Q726b4 homo sapien
16	1476.5	59.8	470	2 Q6ZRU4_HUMAN	Q6zru4 homo sapien
17	1472.5	59.6	470	2 Q495N2_HUMAN	Q495n2 homo sapien
18	1450.5	58.7	477	2 Q4V8B1_RAT	Q4v8b1 rattus norv
19	1447	58.6	511	2 Q495N3_HUMAN	Q495n3 homo sapien
20	1416.5	57.4	477	2 Q811P0_MOUSE	Q811p0 mus musculus
21	1415.5	57.3	477	2 Q8CH37_MOUSE	Q8ch37 mus musculus
22	1351	54.7	490	2 Q454AT_TETNG	Q454at tetraodon n
23	1301	52.7	455	2 Q6ZMU7_HUMAN	Q6zmu7 mus musculus
24	1275.5	51.7	500	2 Q8C077_MOUSE	Q8c077 mus musculus
25	1265.5	51.3	500	2 Q8CH36_MOUSE	Q8ch36 mus musculus
26	1255.5	50.9	504	2 Q6YBV0_HUMAN	Q6ybv0 homo sapien
27	1253	50.7	510	2 Q6DDP2_XENLA	Q6ddp2 xenopus lae
28	1253	50.7	522	2 Q4KL91_XENLA	Q4kl91 xenopus lae
29	1244.5	50.4	504	2 Q86X30_HUMAN	Q86x30 homo sapien
30	1080	43.7	285	2 Q495M4_HUMAN	Q495m4 homo sapien
31	1060.5	43.0	301	2 Q5R828_PONPY	Q5r828 pongo pygma

RESULT 1									
S36A1_HUMAN									
ID	S36A1_HUMAN	STANDARD;							
AC	Q722H8; Q7Z7C0; Q96M74;	PRT;	476	AA.					
DT	16-AUG-2004, integrated into UniProtKB/Swiss-Prot.								
DT	01-OCT-2003, sequence version 1.								
DT	07-MAR-2006, entry version 20.								
DE	Proton-coupled amino acid transporter 1 (Proton/amino acid transporter								
DE	1) (Solute carrier family 36 member 1).								
GN	Name=SLC36A1; Synonyms=PAT1;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;								
OC	Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).								
RA	Chen Z., Fei Y.-J., Huang W., Anderson C.M.H., Wake K.A.,								
RA	Thwaites D.T., Ganapathy V.;								
RT	"Structure and function of a proton-coupled amino acid transporter								
RT	(hPAT1) cloned from the human intestinal cell line Caco2."								
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.								
[2]									
RN	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), AND FUNCTION.								
RC	TISSUE=Intestine;								
RX	MEDLINE=22694810; PubMed=12809675; DOI=10.1016/S0888-7543(03)00099-5;								
RA	Boll M., Foltz M., Rubio-Aliaga I., Daniel H.;								
RT	"A cluster of proton/amino acid transporter genes in the human and								
RL	mouse genomes."								
[3]									
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).								
RC	TISSUE=Endometrial tumor;								
RG	The German cDNA consortium;								
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.								
[4]									
RN	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).								
RC	TISSUE=Testis;								
RX	PubMed=14702039; DOI=10.1038/ng1285;								
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,								
RA	Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,								
RA	Sekine M., Oabayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,								
RA	Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,								
RA	Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,								
RA	Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,								
RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,								
RA	Abe K., Kamiyama K., Katsuta N., Sato K., Tanikawa M., Yamazaki K.,								
RA	Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,								
RA	Tanai H., Kinata M., Watanabe M., Hiraoaka S., Chiba Y., Ishida S.,								
RA	Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,								
RA	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,								
RA	Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,								
RA	Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,								
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,								

Q8n8s6 homo sapien
Q8bub0 mus musculus
Q8msr2 drosophila
Q9vlm3 drosophila
Q7kti1 drosophila
Q9vlm4 drosophila
Q7q4m8 anopheles g
Q5f228 mus musculus
Q7qfg5 anopheles g
Q7pm43 anopheles g
Q495m6 homo sapien
Q7q199 anopheles g
Q8mu61 acyrthosiph
Q9vx84 drosophila

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; As_trans_1.
SQ SEQUENCE 476 AA; 53063 MW; 6485B3BFB94C8EF8 CRC64;

Query Match 98.8%; Score 2439; DB 2; Length 476;
Best Local Similarity 98.3%; Pred. No. 1.4e-168;
Matches 468; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MSTQRLNEDYHDYSDTSDVSPESSEGLNNLSSPGSYQRFQGSNTTWFQTLIHLKGN 60
DB 1 MSTQRLNEDYHDYSDTSDVSPESSEGLNNLSSPGSYQRFQGSNTTWFQTLIHLKGN 60

QY 61 IGTGLLGLPLAVKNGAGIWMGPISLLIIGIVAVHCGILVKCAHFCRLNKFVVDYGDVT 120
DB 61 IGTGLLGLPLAVKNGAGIWMGPISLLIIGIVAVHCGILVKCAHFCRLNKFVVDYGDVT 120

QY 121 MYGLESPCSWLNRNHAHGRVVDFFLIQTQGFCCVYFVLADNFKQVIEAANGTTNCC 180
DB 121 MYGLESPCSWLNRNHAHGRVVDFFLIQTQGFCCVYFVLADNFKQVIEAANGTTNCC 180

QY 161 HNETVILPTWDSRLYMLSFPLFVLVFNRLRALSFSLANITMLVSLVMIYQFIV 240
DB 161 HNETVILPTWDSRLYMLSFPLFVLVFNRLRALSFSLANITMLVSLVMIYQFIV 240

QY 241 QRIQDPDPSHLPLVAPWKTYPFLFGTAIFSGFEGIGWVLPLENKMKDPRKPLIILYLGWIVT 300
DB 241 QRIQDPDPSHLPLVAPWKTYPFLFGTAIFSGFEGIGWVLPLENKMKDPRKPLIILYLGWIVT 300

QY 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFVVP AEIIP 360
DB 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFVVP AEIIP 360

QY 361 FVSRAPHECELVDLFWRTVLVCLTCLAILIPLDLVLSLVGSSSALALIIPPLE 420
DB 361 FVSRAPHECELVDLFWRTVLVCLTCLAILIPLDLVLSLVGSSSALALIIPPLE 420

QY 421 VTFYSEGMSPLTIKDALISILGFGVGVGYEALYELIOPSNAPIFINSTCAFI 476
DB 421 VTFYSEGMSPLTIKDALISILGFGVGVGYEALYELIOPSNAPIFINSTCAFI 476

RESULT 3
Q2VPS4 RABIT PRELIMINARY; PRT; 475 AA..
AC -Q2VPS4;
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 10-JAN-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Proton/amino acid transporter 1.
GN Name=PATI;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Miyauchi S., Abbot E.L., Zhuang L., Subramanian R.K., Ganapathy V.,
RA Thwaites D.T.;
RT "Isolation and function of rabbit PAT1 (slc36a1) and coexpression with
RT the IMINO transporter in renal brush-border membrane vesicles";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY989816; AAY42402.1; -; mRNA.
SQ SEQUENCE 475 AA; 52701 MW; A66BB738C7D2B27F CRC64;

Query Match 93.9%; Score 2317.5; DB 2; Length 475;

Best Local Similarity 92.2%; Pred. No. 9.3e-160;
Matches 439; Conservative 23; Mismatches 13; Indels 1; Gaps 1;

QY 1 MSTQRLNEDYHDYSDTSDVSPESSEGLNNLSSPGSYQRFQGSNTTWFQTLIHLKGN 60
DB 1 MSTQRLNEDYHDYSDTSDVSPESSEGLNNLSSPGSYQRFQGSNTTWFQTLIHLKGN 59

QY 61 IGTGLLGLPLAVKNGAGIWMGPISLLIIGIVAVHCGILVKCAHFCRLNKFVVDYGDVT 120
DB 61 IGTGLLGLPLAVKNGAGIWMGPISLLIIGIVAVHCGILVKCAHFCRLNKFVVDYGDVT 119

QY 121 MYGLESPCSWLNRNHAHGRVVDFFLIQTQGFCCVYFVLADNFKQVIEAANGTTNCC 180
DB 121 MYGLESPCSWLNRNHAHGRVVDFFLIQTQGFCCVYFVLADNFKQVIEAANGTTNCC 179

QY 161 HNETVILPTWDSRLYMLSFPLFVLVFNRLRALSFSLANITMLVSLVMIYQFIV 240
DB 161 HNETVILPTWDSRLYMLSFPLFVLVFNRLRALSFSLANITMLVSLVMIYQFIV 239

QY 241 QRIQDPDPSHLPLVAPWKTYPFLFGTAIFSGFEGIGWVLPLENKMKDPRKPLIILYLGWIVT 300
DB 241 QRIQDPDPSHLPLVAPWKTYPFLFGTAIFSGFEGIGWVLPLENKMKDPRKPLIILYLGWIVT 299

QY 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFVVP AEIIP 360
DB 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFVVP AEIIP 359

QY 361 FVSRAPHECELVDLFWRTVLVCLTCLAILIPLDLVLSLVGSSSALALIIPPLE 420
DB 361 FVSRAPHECELVDLFWRTVLVCLTCLAILIPLDLVLSLVGSSSALALIIPPLE 419

QY 421 VTFYSEGMSPLTIKDALISILGFGVGVGYEALYELIOPSNAPIFINSTCAFI 476
DB 421 VTFYSEGMSPLTIKDALISILGFGVGVGYEALYELIOPSNAPIFINSTCAFI 475

RESULT 4
S36A1 RAT STANDARD; PRT; 475 AA..
AC Q924A5;
DT 16-AUG-2004, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DT 07-MAR-2006, entry version 23.
DE Proton-coupled amino acid transporter 1 (Proton/amino acid transporter
DE 1) (Solute carrier family 36 member 1) (lysosomal amino acid
DE transporter 1) (LYAAT-1) (Neutral amino acid/proton symporter).
GN Name=Slc36a1; Synonyms=Lyaaat1, Pat1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC STRAIN=Sprague-Dawley; TISSUE=Hippocampus;
RX MEDLINE=2130917; PubMed=11390972; DOI=10.1073/pnas.121183498;
RA Sagne C., Agulhon C., Ravassard P., Darmon M., Hamon M.,
RA El Mestikawy S., Gashier B., Giros B.;
RT "Identification and characterization of a lysosomal transporter for
RT small neutral amino acids";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7206-7211(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Brain;
RX PubMed=12598615;
RA Wreden C.C., Johnson J., Tran C., Seal R.P., Copenhagen D.R.,
RA Reimer R.J., Edwards R.H.;
RT "The H-coupled electrogenic lysosomal amino acid transporter LYAAT1
RT localizes to the axon and plasma membrane of hippocampal neurons";
RL J. Neurosci. 23:1265-1275(2003).
CC -!- FUNCTION: Neutral amino acid/proton symporter. Probably involved

CC in the efflux of lysosomal proteolysis products such as L-proline,
CC L-alanine and glycine from the cell. May play a role in specifying

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal and
CC plasma membrane. In neurons, colocalizes with the exocyst complex
CC in the axonal processes.

CC -1- TISSUE SPECIFICITY: Widely expressed and predominantly expressed
CC in brain. Within the brain, expression restricted to neurons and
CC not detected in glial cells. Abundant in regions rich in neurons
CC using glutamate and GABA such as Purkinje cells in the cerebellum
CC and pyramidal cells in the hippocampus.

CC -1- SIMILARITY: Belongs to the amino acid/polyamine transporter 2
CC family.

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CC -----

DR EMBL; AF361239; AAK67316.1; -; mRNA.

DR Ensembl; ENSRNOG0000012356; Rattus norvegicus.

DR RGD; 619801; Slc36a1.

DR -GO; GO:0005764; C:lysosome; IDA.

DR -GO; GO:0005886; C:plasma membrane; IDA.

DR -GO; GO:0015078; F:hydrogen ion transporter activity; IDA.

DR -GO; GO:0015175; F:neutral amino acid transporter activity; IDA.

DR -GO; GO:0015804; P:neutral amino acid transport; IDA.

DR -GO; GO:0015992; P:proton transport; IDA.

DR InterPro; IPR002422; AA/rel_permease2.

DR Pfam; PF01490; Aa_trans_1.

KW Amino-acid transport; Glycoprotein; Membrane; Symport; Transmembrane;
KW Transport.

FT CHAIN 1 475 Proton-coupled amino acid transporter 1.
FT /FTID=PRO 0000093827.

FT TRANSMEM 51 71 Potential.

FT TRANSMEM 78 98 Potential.

FT TRANSMEM 141 161 Potential.

FT TRANSMEM 190 210 Potential.

FT TRANSMEM 215 235 Potential.

FT TRANSMEM 257 277 Potential.

FT TRANSMEM 289 309 Potential.

FT TRANSMEM 342 362 Potential.

FT TRANSMEM 372 392 Potential.

FT TRANSMEM 397 417 Potential.

FT TRANSMEM 439 459 Potential.

FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 469 469 N-linked (GlcNAc...) (Potential).

FT CONFLICT 108 108 L -> M (in Ref. 2).

SQ SEQUENCE 475 AA; 52569 MW; D3D04A489AD1D23C CRC64;

Query Match

Best Local Similarity 86.9%; Score 2146.5; DB 1; Length 475;

Matches 408; Conservative 36; Mismatches 31; Indels 1; Gaps 1;

QY 1 MSTORLNEVDHYSSTDVSPSPGLNLLSPGSGYRFGQSNSTWFTQTLHLKGN 60

DB 1 MSTORLNEVDHYSSTDVSPSPSPGLGSGF-SPGSGYRFGQSNSTWFTQTLHLKGN 59

QY 61 IGTGLGLGLAVKNAGVIMGPIISLIIGIVAVHGMGILVKCAHHFCRLNKSFDYDGTV 120

DB 60 IGTGLGLGLAVKNAGLLGLSLVIGIVAVHGMGILVKCAHLCRLNKPFLDYDGTV 119

QY 121 MYGLESPCSWLNRHAWHGRVDFPFLIVTQLGCCYFFFLADNFQVIEAANGTTNC 180

DB 120 MYGLESPSTWIRNHSWGRVDFPFLVWTQLGCCYFFFLADNFQVIEAANGTTNC 179

QY 181 HNNETVILTPMDSRLYMLSLPFLVLLVFLTRNLRLSIFSLLANITWLSLVMIYQFIV 240

DB 180 NNNETVILTPMDSRLYMLTFLPFLVLLSFLTRNLRLSIFSLLANISMFVSLMIYQFIV 239

QY 241 QRIPDPHSLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKKQDKPRKPLILYLGMVIT 300

Db 240 QRIPDPHSLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKKQDKSPKPLILYLGMVIT 299
QY 301 ILYISGCGLYQFGANIGSITLNPNCWLYOSVKLYSIGIFFTYALQFYVPAEIIIP 360
Db 300 ILYISGSLGYLQFGADIKGSITLNPNCWLYOSVKLYSIGIFFTYALQFYVPAEIIIP 359
QY 361 FVVSRAPEHCELVDFVFTVLVCLTCLAILLPRDLVLSLVGSSSSSALALIIPLE 420
Db 360 AIVSRVPEFELVDSLARTAMCVTCVLAVLPRDLVLSLVGSSSSSALALIIPLE 419
QY 421 VTFYSEGSPITIPKDALISILGFGVGVVGTVEALYELIQPSNAPIFINSTCAFI 476
Db 420 VTFYSEGSPITITKDALISILGFGVGVVGTVEALYELIQPSNASTSAFI 475

RESULT 5

S36A1_MOUSE

ID S36A1_MOUSE STANDARD; PRT; 475 AA.

AC Q8K4D3; Q8LI19;

DT 16-AUG-2004, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2002, sequence version 1.

DT 07-MAR-2006, entry version 21.

DE Proton-coupled amino acid transporter 1 (Proton/amino acid transporter

DE 1) (Solute carrier family 36 member 1).

GN Name=Slc36a1; Synonyms=Pat1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.

RC STRAIN=C57BL/6;

RX MEDLINE=22063354; PubMed=11959859; DOI=10.1074/jbc.M200374200;

RA Boll M., Foltz M., Rubio-Aliaja I., Kortra G., Daniel H.;

RT "Functional characterization of two novel mammalian electrogenic

RT proton-dependent amino acid cotransporters.";

RL J. Biol. Chem. 277:22966-22973(2002).

RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA].

RX PubMed=15058382; DOI=10.1007/s00335-003-2319-3;

RA Birmingham J.R. Jr., Pennington J.;

RT "Organization and expression of the SLC36 cluster of amino acid

RT transporter genes.";

RL Mamm. Genome 15:114-125(2004).

CC -1- FUNCTION: Neutral amino acid/proton symporter. Has a pH-dependent

CC electrogenic transport activity for small amino acids such as

CC glycine, alanine and proline. Besides small apolar L-amino acids,

CC it also recognizes their D-enantiomers and selected amino acid

CC derivatives such as gamma-aminobutyric acid.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal and

CC plasma membrane (By similarity).

CC -1- TISSUE SPECIFICITY: Highly expressed in small intestine, colon,

CC kidney and brain.

CC -1- SIMILARITY: Belongs to the amino acid/polyamine transporter 2

CC family.

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CC -----

DR EMBL; AF453743; AAM80480.1; -; mRNA.

DR EMBL; AY211262; AAC37090.1; -; mRNA.

DR Ensembl; ENSMUSG0000020261; Mus musculus.

DR MGI; MGI:2445299; Slc36a1

DR GO; GO:0015187; F:glycine transporter activity; IDA.

DR GO; GO:0015180; F:L-alanine transporter activity; IDA.

DR GO; GO:0015193; F:L-proline transporter activity; IDA.

DR GO; GO:0015816; P:glycine transport; IDA.

DR GO; GO:0015808; P:L-alanine transport; IDA.

DR GO; GO:0015824; P:L-proline transport; IDA.

DR GO; GO:0015992; P:proton transport; IDA.

DR InterPro; IPR002422; AA/rel_permease2.

```
DR InterPro; IPR013057; AA transp_TM.
KW Pfam; PF01490; AA trans; 1.
KW Amino-acid transport; Glycoprotein; Membrane; Symport; Transmembrane;
KW Transport.
FT CHAIN 1 475 Proton-coupled amino acid transporter 1.
FT /FTID=PRO_0000093826.
FT TRANSMEM 51 71 Potential.
FT TRANSMEM 78 98 Potential.
FT TRANSMEM 141 161 Potential.
FT TRANSMEM 190 210 Potential.
FT TRANSMEM 215 235 Potential.
FT TRANSMEM 257 277 Potential.
FT TRANSMEM 289 309 Potential.
FT TRANSMEM 342 362 Potential.
FT TRANSMEM 372 392 Potential.
FT TRANSMEM 397 417 Potential.
FT TRANSMEM 439 459 Potential.
FT CARBOHYD 43 43 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 133 133 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 182 182 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 469 469 N-linked (GlcNAc...) (Potential).
FT CONFLICT 43 43 N -> S (in Ref. 2).
FT CONFLICT 198 198 L -> P (in Ref. 2).
SQ SEQUENCE 475 AA; 52466 MW; 113C23309F2B51F1 CRC64;

Query Match 86.7%; Score 2141.5; DB 1; Length 475;
Best Local Similarity 85.9%; Pred. No. 5.5e-147;
Matches 409; Conservative 33; Mismatches 33; Indels 1; Gaps 1;

QY 1 MSTQRLNEDYHDSSTDVSPSESEGLNLSFGSYQRFQSGNSTTWFQTLIHLKGN 60
DB 1 MSTQRLNEDYHDSSTDVSPSESEGLNLSFGSYQRFQSGNSTTWFQTLIHLKGN 59

QY 61 IGTGLGLPLAVKNGIYVGPISLLIIGIVAVHCHGILVKAHHFCRLNKSFDYDGT 120
DB 60 IGTGLGLPLAVKNGIYVGPISLLIIGIVAVHCHGILVKAHHFCRLNKSFDYDGT 119

QY 121 MYGLESPCSMLRNHAGHRRVDFLLVLTQLGCCVYFVLADNFKQVIEAANGTTNCC 180
DB 120 MYGLESPCSMLRNHAGHRRVDFLLVLTQLGCCVYFVLADNFKQVIEAANGTTNCC 179

QY 181 HNNETVILPTMDSRLYMLSPFLVLLVFIIRNLRLSIFSLANITMLVSLVMIYQFIV 240
DB 180 NNNVTIPTMDSRLYMLSPFLVLLVFIIRNLRLSIFSLANISMFVSLMIYQFIV 239

QY 241 QRIPDPHPLVAPWKTYPLFFGTAFIFSEGIGMVLPLENKKDKPRKPLIYLGMVIT 300
DB 240 QRIPDPHPLVAPWKTYPLFFGTAFIFSEGIGMVLPLENKKDKSKPFLLIYLGMVIT 299

QY 301 ILVYSLGCLGYLQFANIGSITLNLPCNWLQYQSVKLLYSIGIFFTYALQFVPAEIIIP 360
DB 300 VLYISLGLGYLQFANIGSITLNLPCNWLQYQSVKLLYSIGIFFTYALQFVPAEIIIP 359

QY 361 FVFSRAPHCHELVDFVRLVCLTCLAILIPRLDLVISLVGSSSSALALIIPPLLE 420
DB 360 AIVSRVPEHFLMWDLVLRVTAMVCVCLAILIPRLDLVISLVGSSSSALALIIPPLLE 419

QY 421 VTTYFSEGMSPLTIKDALISILGFVGVGTGYEALYELIQSPNAPIFINSTCAFI 476
DB 420 VVTYVYEGISPLTVTKDALISILGFVGVGTGYEALYELIQSPNAPIFINSTSAFI 475

RESULT 6
Q5F227 MOUSE
ID Q5F227 MOUSE PRELIMINARY; PRT; 475 AA.
AC Q5F227.
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DE Solute carrier family 36 (proton)/amino acid symporter, member 1.
GN Name=SLC36A1; ORFNames=RP24-239D8.3-001;
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Phillimore B.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AL713870; CA152048.1; -; Genomic DNA.
DR GO; ENSMUSG00000020261; Mus musculus.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR013057; AA_transp_TM.
DR Pfam; PF01490; Aa_trans; 1.
SQ SEQUENCE 475 AA; 52466 MW; 113C23309F2B51F1 CRC64;

Query Match 86.7%; Score 2141.5; DB 2; Length 475;
Best Local Similarity 85.9%; Pred. No. 5.5e-147;
Matches 409; Conservative 33; Mismatches 33; Indels 1; Gaps 1;

QY 1 MSTQRLNEDYHDSSTDVSPSESEGLNLSFGSYQRFQSGNSTTWFQTLIHLKGN 60
DB 1 MSTQRLNEDYHDSSTDVSPSESEGLNLSFGSYQRFQSGNSTTWFQTLIHLKGN 59

QY 61 IGTGLGLPLAVKNGIYVGPISLLIIGIVAVHCHGILVKAHHFCRLNKSFDYDGT 120
DB 60 IGTGLGLPLAVKNGIYVGPISLLIIGIVAVHCHGILVKAHHFCRLNKSFDYDGT 119

QY 121 MYGLESPCSMLRNHAGHRRVDFLLVLTQLGCCVYFVLADNFKQVIEAANGTTNCC 180
DB 120 MYGLESPCSMLRNHAGHRRVDFLLVLTQLGCCVYFVLADNFKQVIEAANGTTNCC 179

QY 181 HNNETVILPTMDSRLYMLSPFLVLLVFIIRNLRLSIFSLANITMLVSLVMIYQFIV 240
DB 180 NNNVTIPTMDSRLYMLSPFLVLLVFIIRNLRLSIFSLANISMFVSLMIYQFIV 239

QY 241 QRIPDPHPLVAPWKTYPLFFGTAFIFSEGIGMVLPLENKKDKPRKPLIYLGMVIT 300
DB 240 QRIPDPHPLVAPWKTYPLFFGTAFIFSEGIGMVLPLENKKDKSKPFLLIYLGMVIT 299

QY 301 ILVYSLGCLGYLQFANIGSITLNLPCNWLQYQSVKLLYSIGIFFTYALQFVPAEIIIP 360
DB 300 VLYISLGLGYLQFANIGSITLNLPCNWLQYQSVKLLYSIGIFFTYALQFVPAEIIIP 359

QY 361 FVFSRAPHCHELVDFVRLVCLTCLAILIPRLDLVISLVGSSSSALALIIPPLLE 420
DB 360 AIVSRVPEHFLMWDLVLRVTAMVCVCLAILIPRLDLVISLVGSSSSALALIIPPLLE 419

QY 421 VTTYFSEGMSPLTIKDALISILGFVGVGTGYEALYELIQSPNAPIFINSTCAFI 476
DB 420 VVTYVYEGISPLTVTKDALISILGFVGVGTGYEALYELIQSPNAPIFINSTSAFI 475

RESULT 7
Q495M3 HUMAN
ID Q495M3 HUMAN PRELIMINARY; PRT; 483 AA.
AC Q495M3.
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DE Solute carrier family 36 (proton)/amino acid symporter, member 2.
GN Name=SLC36A2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
```

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RN RP NUCLEOTIDE SEQUENCE.
RX TISSUE=PCR rescued clones; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA MDLINE=22388257; Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Ustin T.B., Toehiyuki S., Carninci P., Scheetz T.E.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Bosak S.A., Morley P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Wozney K.C., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN RP NUCLEOTIDE SEQUENCE.
RX TISSUE=PCR rescued clones;
RA NIH MGC Project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; BC101103; AA101104.1; -; mRNA.
DR EMBL; BC101101; AA101102.1; -; mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR Pfam; PF01490; Aa trans; 1.
SQ SEQUENCE 483 AA; 53216 MW; E283B8C6FC0C3666 CRC64;

Query Match 69.8%; Score 1722.5; DB 2; Length 483;
Best Local Similarity 71.9%; Pred. No. 1.4e-116;
Matches 340; Conservative 50; Mismatches 62; Indels 21; Gaps 4;

QY 2 STORLNEYDHYDYSSTDVSPSESPSE--GLNNLSSPGSYQRFQGSNSTTTFQTLHLKLG 59
DB 26 SAKLENDK-----STFL--DESPSESAGLK-----KTKGITVFQALHLVKG 66
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DB 67 NMGTGILGLPLAVKNAGILMGPLSLVGMGFACHMILVKCAQRFCKRLNKPMDYGD 126
QY 120 VMYGLESSPCSWLRNHAHGWRRVVDPLIVTQGFCCVYFVLADNPKQVIEAANGTNN 179
DB 127 VMHGLEANPNLQNAHGWRRHVSFFLIITQLGFCVYFVLADNKLQVVEAVNSTNN 186
QY 180 CHNNETVILPTMDSRLYMUSFLPFLVLLVIRNLRLTIFSMLANISMLVSLVLIQYI 239
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QY 240 VQRIPOPSHPLVAPWKTYPLFFGTATFSPFEGIGMVLPLENKMCKPRKFFLILYGMVIV 299
DB 247 TQEIPOPSRPLVASWKTYPLFFGTATFSPFEGIGMVLPLENKMCKNARHFFAILSLGMSIV 306
QY 300 TILYISLCGLYLOFGANIQGSITLNPNCWLYQSVKLLYSIGIFFTYALQFYVPAEIII 359
DB 307 TSLYIGMAALYFRGDDIKASISINLPCWLYQSVKLLYTAGLCTYALQFYVPAEIII 366
QY 360 PFFVSRAPHECHLVVDLFRVTLVCLTICLAILPRDLVLSIVGSSSALALIIPPLL 419
DB 367 PFAISRSTRWALPDLISIRLVWVCLTCLLAILPRDLVLSIVGSSVGTALALIIPPLL 426
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QY 420 EVTTFYSEGMSPLTIKDALISILGFGVFGVGYEALYELIQSNAPIFINST 472
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RESULT 8
Q6ZWK5_HUMAN PRELIMINARY; PRT; 483 AA.
AC Q6ZWK5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 13.
DE CDNA FLJ16051 fis, clone KIDNE2000832.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
RA Masuho Y., Nagai K., Isozaki T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AK122630; BAC85496.1; -; mRNA.
DR Ensembl; ENSG00000186335; Homo sapiens.
DR HGNC; HGNC:18762; SLC36A2.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR013057; AA_transpt_1M.
DR Pfam; PF01490; Aa trans; 1.
SQ SEQUENCE 483 AA; 53244 MW; B29A1671ED6C867D CRC64;

Query Match 69.4%; Score 1713.5; DB 2; Length 483;
Best Local Similarity 71.5%; Pred. No. 6.3e-116;
Matches 338; Conservative 51; Mismatches 63; Indels 21; Gaps 4;

QY 2 STORLNEYDHYDYSSTDVSPSESPSE--GLNNLSSPGSYQRFQGSNSTTTFQTLHLKLG 59
DB 26 SAKLENDK-----STFL--DESPSESAGLK-----KTKGITVFQALHLVKG 66
QY 60 NIGTGLGLPLAVKNAGIVMGPISLLIIGIVAVHVMGILVKCAHFCRRLNKSPVDYGD 119
DB 67 NMGTGILGLPLAVKNAGILMGPLSLVGMGFACHMILVKCAQRFCKRLNKPMDYGD 126
QY 120 VMYGLESSPCSWLRNHAHGWRRVVDPLIVTQGFCCVYFVLADNPKQVIEAANGTNN 179
DB 127 VMHGLEANPNLQNAHGWRRHVSFFLIITQLGFCVYFVLADNKLQVVEAVNSTNN 186
QY 180 CHNNETVILPTMDSRLYMUSFLPFLVLLVIRNLRLTIFSMLANISMLVSLVLIQYI 239
DB 187 CYSNETVILPTMDSRLYMUSFLPFLVLLVIRNLRLTIFSMLANISMLVSLVLIQYI 246
QY 240 VQRIPOPSHPLVAPWKTYPLFFGTATFSPFEGIGMVLPLENKMCKPRKFFLILYGMVIV 299
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Db 367 PFAISRVRSTRWALPDLISIRLVWVCLTCLAILPRDLVLISLVGSSSGTALALIIPPLL 426
Qy 420 EVTTYFSEGMSPLTFKDALISILGFGVGVGTVEALYELIQPSNAPFINST 472
Db 427 EVPTFYSEGMSPLTFKDALISILGFGVGVGTVEALYELIQPSNAPFINST 479

RESULT 9
Q726B5 HUMAN PRELIMINARY; PRT; 483 AA.
ID Q726B5
AC Q726B5
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Proton/amino acid transporter 2.
GN Name=SLC36A2; Synonyms=PAT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN Nucleotide Sequence.
RP Nucleotide Sequence.
RC Tissue=Testis;
RX MEDLINE=22694810; PubMed=12809675; DOI=10.1016/S0888-7543(03)00099-5;
RA Boll M., Foltz M., Rubio-Aliaja I., Daniel H.;
RT "A cluster of proton/amino acid transporter genes in the human and
RL mouse genomes.";
RL Genomics 82:47-56 (2003).
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CC -----
DR EMBL; AY162214; AA011788.1; -; mRNA.
DR Ensembl; ENSG00000186335; Homo sapiens.
DR LinkHub; Q726B5; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:000279; F:amino acid-polyamine transporter activity; IEA.
DR -GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel permease2.
DR InterPro; IPR013057; AA_transp_TM.
DR Pfam; PF01490; AA_trans; 1.
DR -SEQUENCE 483 AA; 53227 MW; 928CE6C38F56673 CRC64;

Query Match 69.3%; Score 1711.5; DB 2; Length 483;
Best Local Similarity 71.7%; Pred. No. 8.8e-116;
Matches 339; Conservative 49; Mismatches 64; Indels 21; Gaps 4;

Qy 2 STORLNRDHYDSTVDSPESPSE--GLNNLSPGSYQRFQSNSTWTFQTLHLKLG 59
Db 26 SAKKLENDK-----STFL--DESPSESAGLK-----KTKGITVFQALHLVKG 66
Qy 60 NICTGLGLPLAVKNAGIWMGPISLLIIGIVAVHCVKGLVLCVCAHFCRLNKSFDVYGD 119
Db 67 NMGTGILGLPLAVKNAGIWMGPISLLIIGIVAVHCVKGLVLCVCAHFCRLNKSFDVYGD 126
Qy 120 VMYGLSSPCSWLRNHAHGRVVRVDFLLIQLGFCVCCVYFVLADNFKQVTEAANGTNN 179
Db 127 VMHGLEANPNALQNHAGHGHIVSFFLINTQLGFCVCCVYFVLADNFKQVTEAANGTNN 186
Qy 180 CHNNETVILTPMDSRLYMLSPFLVLLVFIPLNRLALSIFSLANITMLVSLVMYIQFI 239
Db 187 CYSNETVILTPMDSRLYMLSPFLVLLVFIPLNRLALSIFSLANITMLVSLVMYIQFI 246
Qy 240 VQRIPDPDPLVAPWKYTPLPFGTAIFSPFGIGMVLPLENKMOKPRKFPILYLGMVIV 299
Db 247 TQEIIPDPDPLVAPWKYTPLPFGTAIFSPFGIGMVLPLENKMOKPRKFPILYLGMVIV 306
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Db 367 PFAISRVRSTRWALPDLISIRLVWVCLTCLAILPRDLVLISLVGSSSGTALALIIPPLL 426
Qy 420 EVTTYFSEGMSPLTFKDALISILGFGVGVGTVEALYELIQPSNAPFINST 472
Db 427 EVPTFYSEGMSPLTFKDALISILGFGVGVGTVEALYELIQPSNAPFINST 479

RESULT 10
Q8BHK3 MOUSE PRELIMINARY; PRT; 478 AA.
ID Q8BHK3
AC Q8BHK3
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Adult male aorta and vein cDNA, RIKEN full-length enriched library,
DE clone:A530067G19 product:similar to LYSSOMAL AMINO ACID TRANSPORTER 1
DE (Tramadorin 1) (Activated spleen cDNA, RIKEN full-length enriched
DE library, clone:F830020M05 product:solute carrier family 36
DE (proton/amino acid symporter), member 2, full insert sequence) (Adult
DE male dienecephalon cDNA, RIKEN full-length enriched library,
DE clone:9330106I21 product:similar to LYSSOMAL AMINO ACID TRANSPORTER
DE 1) (18-day embryo whole body cDNA, RIKEN full-length enriched library,
DE clone:1110065P15 product:solute carrier family 36 (proton/amino acid
DE symporter), member 2, full insert sequence) (Transmembrane domain rich
DE protein).
GN Name=SLC36a2; Synonyms=Tramdi; ORFNames=RP24-239D8.1-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN Nucleotide Sequence.
RP Nucleotide Sequence.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
RC Dienecephalon, and Whole body;
RC Dienecephalon, and Whole body;
RX MEDLINE=92792525; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44 (1999).
RN Nucleotide Sequence.
RP Nucleotide Sequence.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
RC Dienecephalon, and Whole body;
RC Dienecephalon, and Whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Katayama T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Bajic M.J., Wilming L.G., Aidinis V., Allen J.E., Bailey T.L.,
RA Ambesi-Impombato A., Apweiler R., Bersano T., Bono H., Chalk A.M.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgiev-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Huminicki L., Iacono M., Ikeo K., Iwama A., Iwakura H.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mortagui-Tabar S., Mulder N., Nakano N., Nakaguchi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J.F., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
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RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Yamanishi S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlstedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kashiwagi T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
RC Dienecephalon, and Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG _RIKEN Genome Exploration Research Group, and Genome Science Group
RG (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
RC Dienecephalon, and Whole body;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nakado I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gassnerland T., Gariboldi M., Glissi C., Godzik A., Gough J.,
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RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Simple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Varaldo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
RC Dienecephalon, and Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Tovo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
RC Dienecephalon, and Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein,
RC Dienecephalon, and Whole body;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
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RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-Format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
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RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Query Match 68.8%; Score 1699.5; DB 2; Length 478;
Best Local Similarity 72.6%; Pred. No. 6.4e-115;
Matches 329; Conservative 50; Mismatches 67; Indels 7; Gaps 1;


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Qy 20 SPEESPSEGLNLSPPGSGYQRFQGSNSTTFTQTLHLKGNIGTGLGLPLAVKNAGIVM 79
Db 29 SQDPSPPANGSSSESSK-----KTGKITGQTLVHLVKGNGTGILGLPLAVKNAGILM 81
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Db 82 GPLSLLVNGLIACHMHLVRCQRFCHRLNKPMDYGDYVHGLAFSPNWLQNHAWG 141
Qy 140 RRVVDFFLIVTQGFCCVYFVFLADNPKQVTEAANGTNNCHNETVLTITPMDSRLYML 199
Db 142 RRVVSFFLIVTQGFCCVYFVFLADNLKQVVEAVNSTISCHKNETVLTITPMDSRLYML 201
Qy 200 SFLPFLVLLFIRNLRLALSIFSLANITMVLVSLVMIYQFIVQRIIDPSPHLPVAPWKTYT 259
Db 202 SFLPVLGLLVFVRNLRLVLTIFSLANISMLVSLVMIYQIIEIPDASQLPLVASWKTYT 261
Qy 260 LFFGTAFSPSEGLNLSPPGSGYQRFQGSNSTTFTQTLHLKGNIGTGLGLPLAVKNAGIVM 319
Db 262 LFFGTAFSPSEGLNLSPPGSGYQRFQGSNSTTFTQTLHLKGNIGTGLGLPLAVKNAGILM 321
Qy 320 GSITLNLPCNWLQYOSVLLYSGIFFTYVALQFYVPAEIIIPFVSRAPEHCELVDLFR 379
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Qy 380 TVLVCLTCILAILPRDLVLSVSGVSSSSALALIIPPLEVTTFYSGMSPLTIFKDAL 439
Db 382 LALVCLTCMLAILPRDLVLSVSGVSSSSALALIIPPLEVTTFYSGMSPLTIFKDAL 441
Qy 440 ISILGFVGVVGTVEALYELTQPSNAPFINST 472
Db 442 ISILGFVGVVGTVEALYELTQPSNAPFINST 474

RESULT 11
Q8J2FI_MOUSE
ID Q8J2FI_MOUSE PRELIMINARY; PRT; 478 AA.
AC Q8J2FI_MOUSE
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Tramadorin 1 (proton/amino acid transporter 2).
GN Name=Sic36a2; Synonyms=PAT2, Tramd1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN - [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Pou3f1 mutant sciatic nerves;
RX MEDLINE=22339849; PubMed=12451123;
RA Bermingham J.R. Jr., Shumas S., Whisenhunt T., Sirkowski E.E.,
RA O'Connell S., Scherer S.S., Rosenfeld M.G.;
RT "Identification of genes that are downregulated in the absence of the
RT POU domain transcription factor pou3f1 (Oct-6, Tst-1, SCIP) in sciatic
RT nerve.";
RL J. Neurosci. 22:10217-10231(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=22063354; PubMed=11959859; DOI=10.1074/jbc.M200374200;
RA Boll M., Foltz M., Rubio-Aliaga I., Kottar G., Daniel H.;
RT "Functional characterization of two novel mammalian electrogenic
RT proton-dependent amino acid cotransporters.";
RL J. Biol. Chem. 277:22966-22973(2002).
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CC -----
DR EMBL; AF512429; AAM4854.1; -; mRNA.
DR EMBL; AF453744; AAM80481.1; -; mRNA.
DR Ensembl; ENSMUSG00000020264; Mus musculus.
DR MGI; MGI:1891430; Sic36a2.
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DR GO; GO:0016021; C:integral to membrane; RCA.
DR GO; GO:0005886; P:plasma membrane; IDA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; RCA.
DR GO; GO:0015187; F:glycine transporter activity; IDA.
DR GO; GO:0005280; F:hydrogen:amino acid symporter activity; IDA.
DR GO; GO:0015180; F:L-alanine transporter activity; IDA.
DR GO; GO:0015193; F:L-proline transporter activity; IDA.
DR GO; GO:0006865; P:amino acid transport; RCA.
DR GO; GO:0015816; P:glycine transport; IDA.
DR GO; GO:0015808; P:L-alanine transport; IDA.
DR GO; GO:0015824; P:L-proline transport; IDA.
DR GO; GO:0015922; P:proton transport; IDA.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR013057; AA_transp_TM.
DR Pfam; PF01490; Aa_trans; 1.
SQ SEQUENCE 478 AA; 52049 MW; 2EC02C59577BE236 CRC64;

Query Match 68.7%; Score 1696.5; DB 2; Length 478;
Best Local Similarity 72.6%; Pred. No. 1.1e-114;
Matches 329; Conservative 49; Mismatches 68; Indels 7; Gaps 1;

Qy 20 SPEESPSEGLNLSPPGSGYQRFQGSNSTTFTQTLHLKGNIGTGLGLPLAVKNAGIVM 79
Db 29 SQDPSPPANGSSSESSK-----KTGKITGQTLVHLVKGNGTGILGLPLAVKNAGILM 81
Qy 80 GPISLLIIGIVAVHMGILVKCAHFCRLNKSFDYGDYVGYDTPMYGLESPPCSWLNRHAWG 139
Db 82 GPLSLLVNGLIACHMHLVRCQRFCHRLNKPMDYGDYVHGLAFSPNWLQNHAWG 141
Qy 140 RRVVDFFLIVTQGFCCVYFVFLADNPKQVTEAANGTNNCHNETVLTITPMDSRLYML 199
Db 142 RRVVSFFLIVTQGFCCVYFVFLADNLKQVVEAVNSTISCHKNETVLTITPMDSRLYML 201
Qy 200 SFLPFLVLLFIRNLRLALSIFSLANITMVLVSLVMIYQFIVQRIIDPSPHLPVAPWKTYT 259
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Qy 260 LFFGTAFSPSEGLNLSPPGSGYQRFQGSNSTTFTQTLHLKGNIGTGLGLPLAVKNAGIVM 319
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Db 382 LALVCLTCMLAILPRDLVLSVSGVSSSSALALIIPPLEVTTFYSGMSPLTIFKDAL 441
Qy 440 ISILGFVGVVGTVEALYELTQPSNAPFINST 472
Db 442 ISILGFVGVVGTVEALYELTQPSNAPFINST 474

RESULT 12
Q6NRA6_XENLA
ID Q6NRA6_XENLA PRELIMINARY; PRT; 479 AA.
AC Q6NRA6_XENLA
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE MGC84608 protein.
GN Name=MGC84608;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Oocytes;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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Db 325 ASITLNLPNCWLYQSVKLLYVVGILCTHALQFYVPAETIIIPLAVSQVSKRWALPVDLSIR 384
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Db 385 LALVCTVCMALILPRLDVLISVGSVSSSALALIIPLLEVTTFYSGMSPLTIFKDAL 444
Qy 440 ISILGFGVGVGTVEALYVELIQPNAPFINST 472
Db 445 ISILGFGVGVGTQALDELIRSGNSLPSNST 477

RESULT 14
Q86YK4 HUMAN
ID Q86YK4 HUMAN PRELIMINARY; PRT; 313 AA.
AC Q86YK4;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Proton/amino acid transporter 3 (Solute carrier family 36
GN Transmembrane transport protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15058382; DOI=10.1007/s00335-003-2319-3;
RA Bermingham J.R. Jr., Pennington J.;
RT "Organization and expression of the SLC36 cluster of amino acid
RL Mamm. Genome 15:114-125 (2004).
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CC -----
DR EMBL; AY227112; AAO37092.1; -; mRNA.
DR Ensembl; ENSG00000123643; Homo sapiens.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel permealase2.
DR InterPro; IPR013057; AA/rel permealase2.
DR Pfam; PF01490; Aa_trans; 1.
KW Transmembrane.
FT NON TER
SQ -SEQUENCE 313 AA; 34934 MW; EFC510827A574E1C CRC64;
Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-107; Length 313;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 164 DNFKQVIEAANGTNNCHNNEVTILPTPMSRLYMLSPFLVLLVFIINLRALSIFSL 223
Db 1 DNFKQVIEAANGTNNCHNNEVTILPTPMSRLYMLSPFLVLLVFIINLRALSIFSL 60
Qy 224 ANITMLSVLMIYQIVQIRIPDPGSHLPLVAPWKYPLPFGTAIFSFGIGMVLPLENKK 283
Db 61 ANITMLSVLMIYQIVQIRIPDPGSHLPLVAPWKYPLPFGTAIFSFGIGMVLPLENKK 120
Qy 284 DPRPPLILYGMVITLILYSLGCLGYLQFGANIQGSITLNLPCWLYQSVKLLYSIGI 343
Db 121 DPRPPLILYGMVITLILYSLGCLGYLQFGANIQGSITLNLPCWLYQSVKLLYSIGI 180
Qy 344 FFTYALQFYVPAEIIIPFVFSRAPEHCELVVDLFFVTVLVCLTCILAILPRLDVLISLV 403
Db 181 FFTYALQFYVPAEIIIPFVFSRAPEHCELVVDLFFVTVLVCLTCILAILPRLDVLISLV 240
Qy 404 GSVSSSALALIIPLLEVTTFYSGMSPLTIFKDALISILGFGVGVGTVEALYVELIQPS 463
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Qy 464 NAPIFINSTCAPI 476
Db 301 NAPIFINSTCAPI 313

RESULT 15
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AC Q7Z6B4;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Proton/amino acid transporter 3 (Solute carrier family 36
GN Name=SLC36A3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=22694810; PubMed=12809675; DOI=10.1016/S0888-7543(03)00099-5;
RA Boll M., Foltz M., Rubio-Alfaga I., Daniel H.;
RT "A cluster of proton/amino acid transporter genes in the human and
RL mouse genomes."
RN Genomics 82:47-56 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (AUG-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY162215; AAO11789.1; -; mRNA.
DR EMBL; BC101095; AA01096.1; -; mRNA.
DR Ensembl; ENSG00000186334; Homo sapiens.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002422; AA/rel permealase2.
DR InterPro; IPR013057; AA/rel permealase2.
DR Pfam; PF01490; Aa_trans; 1.
SQ SEQUENCE 470 AA; 51735 MW; AA192584E6BFE848 CRC64;
Query Match 59.8%; Score 1476.5; DB 2; Length 470;
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Best Local Similarity 62.2%, Pred. No. 9.5e-99;		
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Qy	6	LRNEDYH-DYSSTDVSPEESPEGLNLSLSPGSYQRFQGSNSTTWFOTLIHLKGNLTGT 64
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Db	120	ETCFNTWLRHAHVGRYTVSELLVITQLGFCSVYFMFADNLQOMVEKAHVTSMICPRE 179
Qy	185	TVIITPTWDSRLYMLSPFLPFLVLVFIIRNLRSALISFLLANITMLVLSLMTIYQFIVORIP 244
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Db	360	QVSESVALFVDLSVRSALVCLTCVSAILIPRLDLVLSLVGSVSSSALALIIPALLEIVIF 419
Qy	425	YSEGMSPLTIPKDALISITLGFVGVGVGHYYEALYELIQPSNAPIFINST 472
Db	420	YSEDMSCVTTAKDMISITVGLLGTIGFTGYQALYELPQPSISHM-ANST 466

Search completed: August 24, 2006, 01:24:53
Job time : 306 secs

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OM protein - protein search, using sw model

Run on: August 24, 2006, 01:25:09 ; Search time 50 Seconds
(without alignments)
833.292 Million cell updates/sec

Title: US-10-679-362-2
Perfect score: 2469
Sequence: 1 MSTQRLNEDYHDYSTDV.....YELIQSNAPIFINSTCAFI 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2217	89.8	434	2	US-10-094-749-3076 Sequence 3076, Ap
2	1293.5	52.4	500	2	US-09-178-093B-26 Sequence 26, Appl
3	1255.5	50.9	485	2	US-10-154-419-92 Sequence 92, Appl
4	251.5	10.2	486	2	US-09-178-093B-1 Sequence 1, Appl
5	229.5	9.3	525	2	US-09-178-093B-2 Sequence 2, Appl
6	215.5	8.7	485	1	US-08-362-512A-2 Sequence 2, Appl
7	215.5	8.7	485	2	US-08-964-939-2 Sequence 2, Appl
8	215.5	8.7	485	2	US-09-854-774-2 Sequence 2, Appl
9	203.5	8.2	108	2	US-09-599-360B-109 Sequence 109, App
10	203	8.2	399	2	US-09-248-796A-20813 Sequence 20813, A
11	202.5	8.2	443	2	US-09-248-796A-20815 Sequence 20815, A
12	197	8.0	447	2	US-09-370-253-10 Sequence 10, Appl
13	196	7.9	150	2	US-09-370-767-43308 Sequence 43308, A
14	187.5	7.6	447	2	US-09-370-253-6 Sequence 6, Appl
15	187	7.6	449	2	US-09-640-419C-24 Sequence 24, Appl
16	185.5	7.5	148	2	US-09-270-767-32811 Sequence 32811, A
17	185.5	7.5	148	2	US-09-270-767-48028 Sequence 48028, A
18	180.5	7.3	418	2	US-09-640-419C-25 Sequence 25, Appl
19	179.5	7.3	493	1	US-08-362-512A-4 Sequence 4, Appl
20	179.5	7.3	493	2	US-08-964-939-4 Sequence 4, Appl
21	179.5	7.3	493	2	US-09-854-774-4 Sequence 4, Appl
22	178.5	7.2	456	2	US-09-976-594-584 Sequence 584, App
23	173.5	7.0	446	2	US-09-640-419C-26 Sequence 26, Appl
24	173	7.0	287	2	US-09-248-796A-20822 Sequence 20822, A
25	171.5	6.9	452	2	US-09-640-419C-5 Sequence 5, Appl
26	170	6.9	412	2	US-09-311-021-42 Sequence 42, Appl

ALIGNMENTS

RESULT 1

US-10-094-749-3076
; Sequence 3076, Application US/10094749
; Patent No.-6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO

; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: TSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOPARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO

; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3076
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-094-749-3076

Query Match 89.8%; Score 2217; DB 2; Length 434;

Best Local Similarity 90.8%; Pred. No. 2.4e-221;
Matches 432; Conservative 1; Mismatches 1; Indels 42; Gaps 1;

QY 1 MSTQRLNEDYHDYSTDVSPSESGNLNLSFGSYQRFQGSNSTTWFQTLIHLKGN 60
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QY 61 IGTGLLGLPLAVKNAIGIVMGPIISLIIGIVAHVCMLVKCAHFCRLNKSFDVGDIV 120

Sequence 31761, A
Sequence 46978, A
Sequence 2, Appl
Sequence 27, Appl
Sequence 67, Appl
Sequence 11556, A
Sequence 28, Appl
Sequence 42974, A
Sequence 20816, A
Sequence 37, Appl
Sequence 31638, A
Sequence 46855, A
Sequence 43616, A
Sequence 40, Appl
Sequence 530, Appl
Sequence 32714, A
Sequence 47931, A
Sequence 4, Appl
Sequence 5223, Ap

Db 61 IGTGLLGLPLAAKNAGIWMGPISLLIIGIVAVHCHMGILVKCAHHFCRRLNKSFVDYGDV 120
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Db 181 HNNETVLTPTMDSRLYMLSFPLPLVLLVFIIRNLRLSIFSLLANITMLVSLVMYQFIV 240
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Db 241 QRIIPDPHPLVAPWKTYPLPFGTAIFSPGIGMVLPLENKMCDPRKFPILLYLGMVIT 300
Qy 301 ILXISLGLGYLOFGANIQSITLNLPCNMLYQSVKLLYSIGIFFTYALQFVYPAEIIIP 360
Db 301 ILXISLGLGYLOFGANIQSITLNLPCNMLYQSVKLLYSIGIFFTYALQFVYPAEIIIP 360
Qy 361 FVSRAPHELCVVDLFRVTVCLTCLAILPRDLVLSLGVSSSSALALIIPPLE 420
Db 361 FVSRAPHELCVVDLFRVTVCLTCLAILPRDLVLSLGVSSSSALALIIPPLE 420
Qy 421 VTFYSEGMSPITFKDALISILGFVGVVGTVEALVELIQSNAPIFINSTCAFI 476
Db 421 VTFYSEGMSPITFKDALISILGFVGVVGTVEALVELIQSNAPIFINSTCAFI 476
RESULT 2
US-09-178-093B-26
; Sequence 26, Application US/09178093B
; Patent No. 6660846
; GENERAL INFORMATION:
; APPLICANT: Robert H. Edwards
; APPLICANT: Richard J. Reimer
; APPLICANT: Steve L. McIntire
; APPLICANT: Erik M. Jorgensen
; APPLICANT: Kim Schuske
; TITLE OF INVENTION: Vesicular Amino Acid Transported
; FILE REFERENCE: 2002-0005.30
; CURRENT APPLICATION NUMBER: US/09/178,093B
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/063,012
; PRIOR FILING DATE: 1997-10-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide (RVT2 polypeptide sequence)
US-09-178-093B-26

Query Match 52.4%; Score 1293.5; DB 2; Length 500;
Best Local Similarity 54.7%; Pred. No. 2.2e-125;
Matches 263; Conservative 80; Mismatches 117; Indels 21; Gaps 6;
Qy 6 LRNEDYHDSYSTDVSPSESPSEGLNNLSSPGSYQRFQSNSTTWFTQLIHLKKNIGTGL 65
Db 23 LINEQNFDGSS-----DEEQEQLT--LPQKHQYQLDQ--HGISFVQTLMLHLKKNIGTGL 74
Qy 66 LGPLAVKNAAGIWMGPISLLIIGIVAVHCHMGILVKCAHHFCRRLNKSFVDYGDVVMYGL 125
Db 75 LGPLAIKNAAGIVLGPIISLVFIIISVCHMHILVRCSHFLCQPKKSTGLCYSDTVSFAME 134
Qy 126 SSPCSWLNRHNAHWRVVDFFLIIVTQLGFCVYFVFLADNFKQVIEAANGTT---NCHN 182
Db 135 ASPWSCIQQAAGRSVVDFFLIIVTQLGFCVYFVFLADNFKQVIEAANGTT---NCHN 194
Qy 183 NETVLTPTMDSRLYMLSFPLPLVLLVFIIRNLRLSIFSLLANITMLVSLVMYQFIV 242
Db 195 LSQVCERRSVDLRYMLCFLPLILLVFIIRNLRLSIFSLLANITMLVSLVMYQFIV 254

Qy 243 IPDPSHLPLVAPWKTYPLPFGTAIFSPGIGMVLPLENKMCDPRKFPILLYLGMVITVL 302
Db 255 MPDPHNLPIVAGWKYPLPFGTAIFSPGIGMVLPLENKMCDPRKFPILLYLGMVITVL 314
Qy 303 YISLGLGYLOFGANIQSITLNLPCNMLYQSVKLLYSIGIFFTYALQFVYPAEIIIPF 361
Db 315 YISLGLGYLOFGANIQSITLNLPCNMLYQSVKLLYSIGIFFTYALQFVYPAEIIIPA 374
Qy 362 FVSRAPHELCVVDLFRVTVCLTCLAILPRDLVLSLGVSSSSALALIIPPLEV 421
Db 375 VPARLHAKWKICDFGIRSLVITCAGAVLIIRLDIVISFVCAVSSSTLALILPPLVEI 434
Qy 422 TTFYSEGMSPITFKDALISILGFVGVVGTVEALVELIQSNAPIFINST 472
Db 435 LTFSDKHYNMVLKNISIAFTGFVGLLGTVTVEEIIYPTTAVADGASQSLSLNVNST 494
Qy 473 C 473
Db 495 C 495
RESULT 3
US-10-154-419-92
; Sequence 92, Application US/10154419
; Patent No. 6972187
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Gluckman, Maria Alexandra
; APPLICANT: Meyers, Rachel E.
; TITLE OF INVENTION: NOVEL 38594, 57312, 53659, 57250, 63760, 49938, 32146,
; TITLE OF INVENTION: 57259, 67118, 67067, 62092, 8099, 46455, 54414, 53763,
; TITLE OF INVENTION: 67076, 67102, 44181, 67084FL, 67084ALT, FBH58235FL, 57255,
; TITLE OF INVENTION: AND 57255salt MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-249
; CURRENT APPLICATION NUMBER: US/10/154,419
; CURRENT FILING DATE: 2002-05-22
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Fast-SEQ Version 4.0
; SEQ ID NO 92
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-419-92

Query Match 50.9%; Score 1255.5; DB 2; Length 485;
Best Local Similarity 52.0%; Pred. No. 1.8e-121;
Matches 254; Conservative 80; Mismatches 119; Indels 35; Gaps 6;
Qy 6 LRNEDYHDSYSTDVSPSESPSEGLNNLSSPGSYQRFQSNSTTWFTQLIHLKKNIGTGL 65
Db 7 LINEQNFDGTSDEEHEQE-----LLPVQKHQYQLDQEGISFVQTLMLHLKKNIGTGL 58
Qy 66 LGPLAVKNAAGIWMGPISLLIIGIVAVHCHMGILVKCAHHFCRRLNKSFVDYGDVVMYGL 125
Db 59 LGPLAIKNAAGIVLGPIISLVFIIISVCHMHILVRCSHFLCQPKKSTGLCYSDTVSFAME 118
Qy 126 SSPCSWLNRHNAHWRVVDFFLIIVTQLGFCVYFVFLADNFKOV-----IEAANG 175
Db 119 VSPWSCIQQAAGRSVVDFFLIIVTQLGFCVYFVFLADNFKOV-----IEAANG 178
Qy 176 TTNNCHNNTVLTPTMDSRLYMLSFPLPLVLLVFIIRNLRLSIFSLLANITMLVSLVMI 235
Db 179 SNNPCEER-----SVDLRIYMLCFLPILLVFIIRNLRLSIFSLLANITMLVSLVMI 231
Qy 236 YQFIVQRIIDPSHLPLVAPWKTYPLPFGTAIFSPGIGMVLPLENKMCDPRKFPILLYL 295
Db 232 YQVVRNMPDPHNLPIVAGWKYPLPFGTAIFSPGIGMVLPLENKMCDPRKFPILLYL 291
Qy 296 MVIIVTLYISLGLCYLOFGANIQSITLNLPCNMLYQSVKLLYSIGIFFTYALQFVY 354
Db 292 MGIIVTLYISLGLCYLOFGANIQSITLNLPCNMLYQSVKLLYSIGIFFTYALQFVY 351

Qy 355 AEIIIPFVSRAPEHCELVVDLFTVRLVCLTCILAILPRDLVSLVSGVSSSALALI 414
 Db 352 AEIIIPGITSFHTKWKQICFGIRSLVSLTCAGAILPRDLVIFVGAVSSSTLALI 411
 Qy 415 IPPLEVTTFYSEGMSPITIFKDALISILGFGVGVGYEALYELIQPS-----NAP 466
 Db 412 LPPLVEILTFSKHYNIMWLKNISIAFTGVVGLLGTITVEEIIYPTPKVAGTQSP 471
 Qy 467 IF-INSTC 473
 Db 472 FLNLNSTC 479

RESULT 4
 US-09-178-093B-1
 ; Sequence 1, Application US/09178093B
 ; Patent No. 6660846
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert H. Edwards
 ; APPLICANT: Richard J. Reimer
 ; APPLICANT: Steve L. McIntire
 ; APPLICANT: Erik M. Jorgenson
 ; APPLICANT: Kim Schuske
 ; TITLE OF INVENTION: Vesicular Amino Acid Transported
 ; FILE REFERENCE: 2002-0005.30
 ; CURRENT APPLICATION NUMBER: US/09/178,093B
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR FILING DATE: 1997-10-23
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 486
 ; TYPE: PRT
 ; ORGANISM: Caenorhabditis elegans
 ; FEATURE:
 ; NAME/KEY: CHAIN
 ; LOCATION: (1)...(486)
 ; OTHER INFORMATION: UNC-47 polypeptide sequence
 ; US-09-178-093B-1

Query Match 10.2%; Score 251.5; DB 2; Length 486;
 Best Local Similarity 21.7%; Pred. No. 3.1e-17;
 Matches 107; Conservative 83; Mismatches 171; Indels 131; Gaps 18;
 Qy 22 EESPEGLNNLSSPGSYQRFQGSNTTWFQTLIHLKNGNIGTGLGLPLAVK-----NAG 76
 Db 75 EEAKDDGHGEASEPISA-----LQAANVTNATQGMFIVGLPIAVKVGWWSIG 123
 Qy 77 IVMGPISLIIGIVAVHCGM---ILVKCAHFRCRLNKSFDYDGTVMYGLSSPCSWLR 133
 Db 124 AMVG-----VAYVCYWTGVLLIECLYENGKVKRXTY----- 154
 Qy 134 NHAHGRVVDFF-----LVITQ-----LGFCCVYFVLADNFKQVIEAANGTTNNCHN 182
 Db 155 -----REIADYKPGFKWVLAQAQLTLLSTCIYVLVAD-----LLQSCF- 196
 Qy 183 NETVILPTMDSRLYMLSFPLVLLVFIENLRALSIFSLANIT-MLVSLVMIYQFTIVQ 241
 Db 197 -----PSVDKAGMMITSAULTCSFLDDLQIVSRLSFFNAISHLVNLIMVLYC--- 246
 Qy 242 RIPDPSHLPLVAPW-----KTYPLFFGTAFISFEGIGMWVPLENKKDKPRKPL 290
 Db 247 -----LSFVSQMSFSTITFSLNITLPTIVGMVVFYGTSHIFLPNLEGNMKNPAQFN 299
 Qy 291 ILYLGMVITVILYISLGLCYLOFGANIQGSITLNLNPNCLYQSVKLLYS-----IGIFT 346
 Db 300 MLKWSHIAAAVFKVVGFMGLFTFGELTQBEISNLPN-----QSPKILVNLIVVKALLS 355
 Qy 347 YALQFYVPAEII-----IPFVSRAPEHCELVVDLFTVRLVCLTCILAILPRL 396

Db 356 YPLPFYAAVQLKNNLFLGYPQTPFTSCYSPDKSLREWAVTLRIILVLFTLVALSVPYL 415
 Qy 397 DLVLSVSGVSSSALALIIPPLEVTTFYSEGMSPITIFK---DALISILGFGVGVGY 453
 Db 416 VELMGLVGNITGTMLSFIWPAFLH--YIKB--KTLNPFKRFDOGIIMGSCVCSGVY 471
 Qy 454 EALYELIQPSNA 465
 Db 472 FSSMELLRAINS 483

RESULT 5
 US-09-178-093B-2
 ; Sequence 2, Application US/09178093B
 ; Patent No. 6660846
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert H. Edwards
 ; APPLICANT: Richard J. Reimer
 ; APPLICANT: Steve L. McIntire
 ; APPLICANT: Erik M. Jorgenson
 ; APPLICANT: Kim Schuske
 ; TITLE OF INVENTION: Vesicular Amino Acid Transported
 ; FILE REFERENCE: 2002-0005.30
 ; CURRENT APPLICATION NUMBER: US/09/178,093B
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR FILING DATE: 1997-10-23
 ; NUMBER OF SEQ ID NOS: 50
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 525
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: CHAIN
 ; LOCATION: (1)...(525)
 ; OTHER INFORMATION: RUNC-47 polypeptide sequence
 ; US-09-178-093B-2

Query Match 9.3%; Score 229.5; DB 2; Length 525;
 Best Local Similarity 22.0%; Pred. No. 6.6e-15;
 Matches 95; Conservative 82; Mismatches 178; Indels 77; Gaps 15;
 Qy 62 GTGLGLPLAVKNAIGVMGPISLLIIGIVAVHCGMLVVKCAHFRCR-----RLNKSFDY 116
 Db 131 GMFVLGLPYAILHGG-YLGLFLIIFAAVCCYTGKILLIACLYEENDEGEVVRVDSYV-- 187
 Qy 117 GDTVMYGLSSPCSWLRNHAHGRVVDFFLIIVTQGLGCCVYFVLADNFKQVIEAANGT 176
 Db 188 -----AIAANACCA--PRFPTLGGRVNVVAQII-ELVMTCILYVVVSGNL----- 228
 Qy 177 TNNCHNETVILPTMDSRLYMLSFPLVLL--VFIRNLALSTFSLANITMLVSLVM 234
 Db 229 ---MYNS-----PFLPVSVQSKWSIIATAVLLPCAFELKNLKAWSKFSLLCTLAHFVNIL 280
 Qy 235 IYQIVORIPDPSHLPLVAPW-----KTYPLFFGTAFISFEGIGMWVPLENKK 283
 Db 281 VIAYCLGRAD-----WAEKVKFYIDVKFPISIGIIVFSYTSQIFLPSLEGNMQ 331
 Qy 284 DPRKFPILYLGWVIVITLYISLGLCYLOFGANIQGSITLNLNPNCLYQSVKLLYSIGI 343
 Db 332 QPSEFHCMMNWTIAACVCLKGLFALVAYLTWADETKEVITDNLPG-----SIRAVVNIFL 386
 Qy 344 ----FFTYALQFYVPAEII-----IPFVSRAPEHCELVV-DLFTVRLVCLTCIL 389
 Db 387 VAKALLSYLPFPFAAVEVLEKSLFQEGSRAPFPACYGGDGRKMGWGLTLCALVVFVTLIM 446
 Qy 390 AILPRDLVLSVSGVSSSALALIIPPLEVTTFYSEGMSPITIFKDALISILGFGVGV 449
 Db 447 AIYVPHFALMGLTGTGAGLCFLPLSLFHLRLWRK-LLWHQVFFDVAIFVIGICSV 505
 Qy 450 VGTVEALYELIQ 461

Db 60 LWAIAQLGWIAGTSILLIFSFITVFTSTMLADCYRAPDPVTGKRNVTYMDVRSYLGGR 119
Qy 125 ESSPCSWLRNHAHGRVDFLLVTLQGLFCVVFVFLADNFKQVIEAANGTTNNCHNE 184
Db 120 KVQLC-----GVAQYGN-----LIGVTGVYITITASISLVAVGK-----SNCPHDK 159
Qy 185 TVILPTMDSRLYMLSPFLPLVLLVFNRLRALSIFSLANI-----FGTAIFSPG 271
Db 160 GHTADCTISNYPYMAVFGIIQVILSQIPNFKLSFLSMAAAMSFTYATIGIGLAIAATVA 219
Qy 227 -----TMLVSLVMYQFIVQRIQIPDPSPHPLVAPWKTYPLF-----FGTAIFSPG 271
Db 220 GGVKGTSMGTAVGVDDVTAQAQKI-----WRSFQAVGDIAPAYATVLLIEIQD 268
Qy 272 IGMVLPLENKMCKPRKPLILYLGWIVITILYISLGLCYLQFGANIGSITLN---LPN 328
Db 269 TLRSSPAENKAM--KRASLV---GVSTTFYILCGCIGYAAFGNAPGDFLTDFGPFEP 323
Qy 329 CWLYQ-----SVKLYSIGIFFTYALQF-----YVPAEIIIPFVSRAPEHCELVV 374
Db 324 FWLIDFANACIAVHLIGAYQVFAQPIQFQVEKKRNYPDNKFTITSEYSVNVVPLGKFN 383
Qy 375 DLP---VRTVLVCTILAILIPLDLVISLVGSSSALALIIPLLEVTTFYSEGMS 431
Db 384 SLFRLVWRTAYVITVVMAMIFPFNFNALGLIGAASFPLTVYFPVEMHIAQTKIKKYS 443
Qy 432 LTI-----FKDALISILGFVGVVG 451
Db 444 RWIAKTMCYVCLIVSLLAAGSIAG 469

RESULT 8

US-09-854-774-2
; Sequence 2, Application US/09854774
; Patent No. 6809233
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Beird
; TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID
; TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS
; CONTAINING A TRANSPORTER AND THEIR USE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,774
; FILING DATE: 14-May-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/964,939
; FILING DATE: 1998-05-28
; APPLICATION NUMBER: US 08/007,636
; FILING DATE: 21-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward A.
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 485 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-854-774-2

Query Match 8.7%; Score 215.5; DB 2; Length 485;

Best Local Similarity 20.0%; Pred. No. 1.7e-13;
Matches 101; Conservative 81; Mismatches 221; Indels 103; Gaps 15;

Qy 8 NEDYHDSSTDSPEESPSSEGLNLSPPGSVQRQGSNSTTWFOTLHLLKGNIGTGLLG 67
Db 5 NTEGHNSTAESDAYTVSDPTKNVDEDEKRTG-----TMLTASAHIIITAVIGSGVLS 59
Qy 68 LPLAVKNAGIVMGPISLIIGIVAVHGMGILVKC---AHHFCCRRLNKSFVDYGDVTMYGL 124
Db 60 LWAIAQLGWIAGTSILLIFSFITVFTSTMLADCYRAPDPVTGKRNVTYMDVRSYLGGR 119
Qy 125 ESSPCSWLRNHAHGRVDFLLVTLQGLFCVVFVFLADNFKQVIEAANGTTNNCHNE 184
Db 120 KVQLC-----GVAQYGN-----LIGVTGVYITITASISLVAVGK-----SNCPHDK 159
Qy 185 TVILPTMDSRLYMLSPFLPLVLLVFNRLRALSIFSLANI-----FGTAIFSPG 271
Db 160 GHTADCTISNYPYMAVFGIIQVILSQIPNFKLSFLSMAAAMSFTYATIGIGLAIAATVA 219
Qy 227 -----TMLVSLVMYQFIVQRIQIPDPSPHPLVAPWKTYPLF-----FGTAIFSPG 271
Db 220 GGVKGTSMGTAVGVDDVTAQAQKI-----WRSFQAVGDIAPAYATVLLIEIQD 268
Qy 272 IGMVLPLENKMCKPRKPLILYLGWIVITILYISLGLCYLQFGANIGSITLN---LPN 328
Db 269 TLRSSPAENKAM--KRASLV---GVSTTFYILCGCIGYAAFGNAPGDFLTDFGPFEP 323
Qy 329 CWLYQ-----SVKLYSIGIFFTYALQF-----YVPAEIIIPFVSRAPEHCELVV 374
Db 324 FWLIDFANACIAVHLIGAYQVFAQPIQFQVEKKRNYPDNKFTITSEYSVNVVPLGKFN 383
Qy 375 DLP---VRTVLVCTILAILIPLDLVISLVGSSSALALIIPLLEVTTFYSEGMS 431
Db 384 SLFRLVWRTAYVITVVMAMIFPFNFNALGLIGAASFPLTVYFPVEMHIAQTKIKKYS 443
Qy 432 LTI-----FKDALISILGFVGVVG 451
Db 444 RWIAKTMCYVCLIVSLLAAGSIAG 469

RESULT 9

US-09-599-3608-109
; Sequence 109, Application US/095993608
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,3608
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pgm
; SEQ ID NO 109
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:

[illegible]

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - protein search, using sw model
Run on: August 24, 2006, 01:25:54 ; Search time 185 Seconds
(without alignments)
1191.839 Million cell updates/sec
Title: US-10-679-362-2
Perfect score: 2469
Sequence: 1 MSTQRLRNEDYHDSSTVS.....YELIQSNAPFINSTCAFI 476
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pap:**
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pap:**
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pap:**
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pap:**
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pap:**
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2469	100.0	476	3	US-09-805-456-2
2	2469	100.0	476	4	US-10-225-810-21
3	2469	100.0	476	4	US-10-679-362-2
4	2460	99.6	496	4	US-10-080-334-22
5	2402.5	97.3	568	4	US-10-332-447-8
6	2398	97.1	500	4	US-10-080-334-20
7	2324	94.1	476	3	US-09-805-456-7
8	2324	94.1	476	4	US-10-679-362-7
9	2217	89.8	434	4	US-10-094-749-3076
10	2217	89.8	434	4	US-10-080-334-137
11	2146.5	86.9	475	4	US-10-080-334-138
12	2139.5	86.7	475	4	US-10-225-810-41
13	2137.5	86.6	475	4	US-10-225-810-18
14	1914	77.5	422	4	US-10-291-737-4
15	1914	77.5	422	4	US-10-365-564-4
16	1722.5	69.8	483	4	US-10-225-810-19
17	1718.5	69.6	483	4	US-10-392-219-2
18	1718.5	69.6	507	4	US-10-467-685-7
19	1696.5	68.7	478	4	US-10-225-810-14
20	1677.5	67.9	481	4	US-10-225-810-22
21	1476.5	59.8	427	4	US-10-225-810-20
22	1448.5	58.7	427	4	US-10-291-737-2
23	1448.5	58.7	427	4	US-10-365-564-2
24	1416.5	57.4	477	4	US-10-225-810-17
25	1263	51.2	263	4	US-10-080-334-24
26	1255.5	50.9	485	4	US-10-055-025-2
27	1255.5	50.9	485	4	US-10-154-419-92

28	1255.5	50.9	485	6	US-11-043-889-52	Sequence 52, Appl
29	1255.5	50.9	504	4	US-10-080-334-139	Sequence 139, App
30	1252.5	50.7	476	4	US-10-168-651-23	Sequence 23, Appl
31	1252.5	50.7	476	4	US-10-755-889-22	Sequence 22, Appl
32	989.5	40.1	443	4	US-10-415-378-10	Sequence 10, Appl
33	972.5	39.4	369	4	US-10-108-260A-3609	Sequence 3609, Ap
34	866	35.1	482	4	US-10-225-810-34	Sequence 34, Appl
35	866	35.1	482	6	US-11-097-143-26835	Sequence 26835, A
36	866	35.1	504	4	US-10-080-334-141	Sequence 141, App
37	861	34.9	404	3	US-09-805-456-4	Sequence 4, Appli
38	861	34.9	404	3	US-09-805-456-5	Sequence 5, Appli
39	861	34.9	404	4	US-10-679-362-4	Sequence 4, Appli
40	861	34.9	404	4	US-10-679-362-5	Sequence 5, Appli
41	861	34.9	483	6	US-11-097-143-26193	Sequence 26193, A
42	861	34.9	486	6	US-11-097-143-31110	Sequence 31110, A
43	857	34.7	165	4	US-10-080-334-140	Sequence 140, App
44	853	34.5	404	4	US-10-291-737-5	Sequence 5, Appli
45	853	34.5	404	4	US-10-365-564-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-805-456-2

; Sequence 2, Application US/0905456

; Publication No. US20030170778A1

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; FILE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL001062

; CURRENT APPLICATION NUMBER: US/09/805,456

; CURRENT FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Human

US-09-805-456-2

Query Match 100.0%; Score 2469; DB 3; Length 476;

Best Local Similarity 100.0%; Pred. No. 1.7e-217;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTQRLRNEDYHDSSTVSSTDVSPSESGNLNLSPPSGSYQRFQGSNSTTTFQTLIHLKGN 60

Db 1 MSTQRLRNEDYHDSSTDVSPSESGNLNLSPPSGSYQRFQGSNSTTTFQTLIHLKGN 60

Qy 61 IGTGLGLPLAVKAGIWMGPISLLIIGIVAVHCGMILVKCAHFCRLNLSFVDYGDIV 120

Db 61 IGTGLGLPLAVKAGIWMGPISLLIIGIVAVHCGMILVKCAHFCRLNLSFVDYGDIV 120

Qy 121 MYGLESPCSMLRNHAHWRGVDFLLIVTQGLFCVYFVLADNFKQVIEAANGTTNNC 180

Db 121 MYGLESPCSMLRNHAHWRGVDFLLIVTQGLFCVYFVLADNFKQVIEAANGTTNNC 180

Qy 181 HNNETVILTPMTDSRLYMLSPFLVLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240

Db 181 HNNETVILTPMTDSRLYMLSPFLVLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240

Qy 241 QRIPDPHSLPLAVPKTYPLFEGTAIFSFEGIGMVLPLENKMOKPRKPLILYLGMVIT 300

Db 241 QRIPDPHSLPLAVPKTYPLFEGTAIFSFEGIGMVLPLENKMOKPRKPLILYLGMVIT 300

Qy 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFVPAEIIIP 360

Db 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFVPAEIIIP 360

Qy 361 FFVSRAPHCBLVDLFRVTVLVCITLAILPRDLVIVSLVGSVSSALAIIPPLLE 420

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Db 361 FFVSRAPEHCELVDLFRVTVLVCILAILPRDLVLSVGSVSSALALIIPPLE 420
Qy 421 VTTFYSEGMSPLTIFFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476
Db 421 VTTFYSEGMSPLTIFFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476

RESULT 2
US-10-225-810-21
; Sequence 21, Application US/10225810
; Publication No. US20030157512A1
; GENERAL INFORMATION:
; APPLICANT: Bebmingham, Jr., John R.
; TITLE OF INVENTION: Tramdorins and Methods of Using Tramdorin
; FILE REFERENCE: McLaugh-07165
; CURRENT APPLICATION NUMBER: US/10/225,810
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-810-21

Query Match 100.0%; Score 2469; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTORLNEDYHDYSSTDVSPSESGNLNLSPPGSGYQRFQGSNSTTWFTLIHLKGN 60
Db 1 MSTORLNEDYHDYSSTDVSPSESGNLNLSPPGSGYQRFQGSNSTTWFTLIHLKGN 60
Qy 61 IGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHGMGLVKCAHFCRRLNKSFVDYGDV 120
Db 61 IGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHGMGLVKCAHFCRRLNKSFVDYGDV 120
Qy 121 MYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Qy 181 HNNETVILPTMDSRLYMLSFPLFVLVLFIRNLRLAISIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNNETVILPTMDSRLYMLSFPLFVLVLFIRNLRLAISIFSLLANITMLVSLVMIYQFIV 240
Qy 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGWVLPLENKMKDPRKPLILYLGWIVT 300
Db 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGWVLPLENKMKDPRKPLILYLGWIVT 300
Qy 301 ILVYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFYVPAEIIIP 360
Db 301 ILVYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFYVPAEIIIP 360
Qy 361 FFVSRAPEHCELVDLFRVTVLVCILAILPRDLVLSVGSVSSALALIIPPLE 420
Db 361 FFVSRAPEHCELVDLFRVTVLVCILAILPRDLVLSVGSVSSALALIIPPLE 420
Qy 421 VTTFYSEGMSPLTIFFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476
Db 421 VTTFYSEGMSPLTIFFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476

RESULT 3
US-10-679-362-2
; Sequence 2, Application US/10679362
; Publication No. US20040146887A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001062CON
; CURRENT APPLICATION NUMBER: US/10/679,362
```

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; CURRENT FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-679-362-2

Query Match 100.0%; Score 2469; DB 4; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTORLNEDYHDYSSTDVSPSESGNLNLSPPGSGYQRFQGSNSTTWFTLIHLKGN 60
Db 1 MSTORLNEDYHDYSSTDVSPSESGNLNLSPPGSGYQRFQGSNSTTWFTLIHLKGN 60
Qy 61 IGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHGMGLVKCAHFCRRLNKSFVDYGDV 120
Db 61 IGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHGMGLVKCAHFCRRLNKSFVDYGDV 120
Qy 121 MYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESSPCSWLRNHAHWGRVVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Qy 181 HNNETVILPTMDSRLYMLSFPLFVLVLFIRNLRLAISIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNNETVILPTMDSRLYMLSFPLFVLVLFIRNLRLAISIFSLLANITMLVSLVMIYQFIV 240
Qy 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGWVLPLENKMKDPRKPLILYLGWIVT 300
Db 241 QRIPDPSHLPLVAPWKTYPLFFGTAFISFEGIGWVLPLENKMKDPRKPLILYLGWIVT 300
Qy 301 ILVYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFYVPAEIIIP 360
Db 301 ILVYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFFTYALQFYVPAEIIIP 360
Qy 361 FFVSRAPEHCELVDLFRVTVLVCILAILPRDLVLSVGSVSSALALIIPPLE 420
Db 361 FFVSRAPEHCELVDLFRVTVLVCILAILPRDLVLSVGSVSSALALIIPPLE 420
Qy 421 VTTFYSEGMSPLTIFFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476
Db 421 VTTFYSEGMSPLTIFFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTCAFI 476

RESULT 4
US-10-080-334-22
; Sequence 22, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
```

;; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
;; FILE OF INVENTION: Using the Same
;; CURRENT APPLICATION NUMBER: US/10/080,334
;; PRIOR FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: 60/270,523
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: 60/322,712
;; PRIOR FILING DATE: 2001-09-17
;; PRIOR APPLICATION NUMBER: 60/311,980
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 60/330,307
;; PRIOR FILING DATE: 2001-10-18
;; PRIOR APPLICATION NUMBER: 60/278,796
;; PRIOR FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: 60/281,521
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/276,677
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/311,595
;; PRIOR FILING DATE: 2001-08-10
;; PRIOR APPLICATION NUMBER: 60/270,220
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: 60/274,295
;; PRIOR FILING DATE: 2001-03-08
;; PRIOR APPLICATION NUMBER: 60/318,526
;; PRIOR FILING DATE: 2001-09-10
;; PRIOR APPLICATION NUMBER: 60/286,548
;; PRIOR FILING DATE: 2001-04-25
;; PRIOR APPLICATION NUMBER: 60/291,765
;; PRIOR FILING DATE: 2001-05-17
;; PRIOR APPLICATION NUMBER: 60/270,797
;; PRIOR FILING DATE: 2001-02-23
;; PRIOR APPLICATION NUMBER: 60/276,400
;; PRIOR FILING DATE: 2001-03-16
;; PRIOR APPLICATION NUMBER: 60/270,810
;; PRIOR FILING DATE: 2001-02-23
;; NUMBER OF SEQ ID NOS: 388
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 22
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-080-334-22

Query Match 99.6%; Score 2460; DB 4; Length 496;
Best Local Similarity 99.8%; Pred. No. 1.2e-216;
Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MSTQRLRNEDYHDSSTDVSPSESGNLNLSPPSGYQRFQGSNSTTWFTQLIHLLKGN 60
Db 21 MSTQRLRNEDYHDSSTDVSPSESGNLNLSPPSGYQRFQGSNSTTWFTQLIHLLKGN 80
Qy 61 GTGGLGLPLAVKAGIWMGPISLLIIGIVAVCHMGILVKCAHFCRRLNKSFDVYDGTV 120
Db 81 GTGGLGLPLAVKAGIWMGPISLLIIGIVAVCHMGILVKCAHFCRRLNKSFDVYDGTV 140
Qy 121 MYGLESPCSWLNRHAGRRVDFFLVLTQLGFCVVYFVLADNFKQVIEAANGTTNCC 180
Db 141 MYGLESPCSWLNRHAGRRVDFFLVLTQLGFCVVYFVLADNFKQVIEAANGTTNCC 200
Qy 181 HNNETVILTPWDSRLYMLSPFLPFLVLLVFNRLNRLAISFSLLANITMLVSLVMIYQFIV 240
Db 201 HNNETVILTPWDSRLYMLSPFLPFLVLLVFNRLNRLAISFSLLANITMLVSLVMIYQFIV 260
Qy 241 QRIPDPShLPVAPWKTYPLFFGTAFISFEGIGMWLPLENKKMDPRKPFLLYLGMWIVT 300
Db 261 QRIPDPShLPVAPWKTYPLFFGTAFISFEGIGMWLPLENKKMDPRKPFLLYLGMWIVT 320
Qy 301 ILYISLGLCYLQFQANITLNPNCWLYQSCKLYSGIIFTYALQFVPAEIIIP 360
Db 321 ILYISLGLCYLQFQANITLNPNCWLYQSCKLYSGIIFTYALQFVPAEIIIP 380

Qy 361 FFVSRAPEHCELVVDLFLVTVLVCLTCLAILPRLDLVLVSLVSSSALALIIPPLLE 420
Db 381 FFVSRAPEHCELVVDLFLVTVLVCLTCLAILPRLDLVLVSLVSSSALALIIPPLLE 440
Qy 421 VTTFYSEGMSPLTIFKDALISILGFGVGVCTYEALYELIOPSNAPIINSTCAFI 476
Db 441 VTTFYSEGMSPLTIFKDALISILGFGVGVCTYEALYELIOPSNAPIINSTCAFI 496
RESULT 5
US-10-332-447-8
;; Sequence 8, Application US/10332447
;; Publication No. US20040053258A1
;; GENERAL INFORMATION:
;; APPLICANT: INCYTE GENOMICS, INC.; RAUMANN, Brigitte E.;
;; APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;
;; APPLICANT: TANG, Y. Tom; HARLAND, Lee; BURFORD, Neil;
;; APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;
;; APPLICANT: BAUGHN, Marian R.; YAO, Monique G.; YANG, Junming;
;; APPLICANT: ARVIZU, Chandra S.; GANDHI, Ameena R.;
;; APPLICANT: HAFALIA, April J.A.; TRIBOULEY, Catherine M.;
;; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Javalaxmi;
;; APPLICANT: LU, Yan; LU, Dyung Aina M.; AZIMZAI, Yalda;
;; APPLICANT: LAL, Preeti; ELLIOTT, Vicki S.; NGUYEN, Damiel B.;
;; APPLICANT: XU, Yuming; SEILHAMER, Jeffrey J.; BOROWSKY, Mark L.;
;; APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELU, Kavitha;
;; APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.
;; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
;; FILE REFERENCE: PI-0149 USN
;; CURRENT APPLICATION NUMBER: US/10/332,447
;; CURRENT FILING DATE: 2003-01-07
;; PRIOR APPLICATION NUMBER: US 60/216,547
;; PRIOR FILING DATE: 2000-07-07
;; PRIOR APPLICATION NUMBER: US 60/218,232
;; PRIOR FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: US 60/220,112
;; PRIOR FILING DATE: 2000-07-21
;; PRIOR APPLICATION NUMBER: US 60/221,839
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PERL Program
;; SEQ ID NO 8
;; LENGTH: 568
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc.feature
;; OTHER INFORMATION: Incyte ID No. US20040053258A1 7476747CD1
US-10-332-447-8

Query Match 97.3%; Score 2402.5; DB 4; Length 568;
Best Local Similarity 98.3%; Pred. No. 2.6e-211;
Matches 474; Conservative 0; Mismatches 2; Indels 61; Gaps 2;
Qy 1 MSTQRLRNEDYHDSSTDVSPSESGNLNLSPPSGYQRFQGSNSTTWFTQLIHLLKGN 60
Db 32 MSTQRLRNEDYHDSSTDVSPSESGNLNLSPPSGYQRFQGSNSTTWFTQLIHLLKGN 91
Qy 61 GTGGLGLPLAVKAGIWMGPISLLIIGIVAVCHMGILVKCAHFCRRLNKSFDVYDGTV 120
Db 92 GTGGLGLPLAVKAGIWMGPISLLIIGIVAVCHMGILVKCAHFCRRLNKSFDVYDGTV 151
Qy 121 MYGLESPCSWLNRHAGRRVDFFLVLTQLGFCVVYFVLADNFKQVIEAANGTTNCC 180
Db 152 MYGLESPCSWLNRHAGRRVDFFLVLTQLGFCVVYFVLADNFKQVIEAANGTTNCC 211
Qy 181 HNNETVILTPWDSRLYMLSPFLPFLVLLVFNRLNRLAISFSLLANITMLVSLVMIYQFIV 240
Db 212 HNNETVILTPWDSRLYMLSPFLPFLVLLVFNRLNRLAISFSLLANITMLVSLVMIYQFIV 271
Qy 241 QRIPDPShLPVAPWKTYPLFFGTAFISFEGIGMWLPLENKKMDPRKPFLLYLGMWIVT 300

Db 272 QRIIDPDLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPKPFLLILVGMVIVT 331
Qy 301 ILVLSGLGVLORGANIQSITLNLPCNLVQSVKLLYSIGIGFFTYALQFYVPAEIIIP 360
Db 332 ILVLSGLGVLORGANIQSITLNLPCNLVQSVKLLYSIGIGFFTYALQFYVPAEIIIP 391
Qy 361 FFVSRAPHELCVVDLFRVTVLCLT----- 386
Db 392 FFVSRAPHELCVVDLFRVTVLCLTSLSGSDVNGMYGTADGTCGSAPLVVFSSFLA 451
Qy 387 -----C----- 419
Db 452 HPMLSFCEGWSCHRDVVVWGFARGILAILIPRLDLVLSVSVSSALALIIPLL 511
Qy 420 EVTTFYSEGMSPLTFKDALISILGFGVGVGTVEALYELIQSNAPIFINSTCAFI 476
Db 512 EVTTFYSEGMSPLTFKDALISILGFGVGVGTVEALYELIQSNAPIFINSTCAFI 568

RESULT 6

US-10-080-334-20
; Sequence 20, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li
; APPLICANT: Shenov, Sureah G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2001-02-21
; PRIOR FILING DATE: 2001-02-21
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 2001-08-13
; PRIOR FILING DATE: 2001-08-13
; PRIOR FILING DATE: 2001-10-18
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2001-04-04
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-03-16
; PRIOR FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2001-02-21
; PRIOR FILING DATE: 2001-02-21
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2001-03-08
; PRIOR FILING DATE: 2001-09-10

; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-334-20

Query Match 97.1%; Score 2398; DB 4; Length 500;
Best Local Similarity 97.5%; Pred. No. 5.8e-211; Mismatches 0; Indels 12; Gaps 3;
Matches 472; Conservative 0

Qy 1 MSTQRLRNEDYHDYSSSTDVSPSPSEGLNNLSPGSGYQRFQSGNSTTWTQTLIHLKGN 60
Db 21 MSTQRLRNEDYHDYSSSTDVSPSPSEGLNNLSPGSGYQRFQSGNSTTWTQTLIHLKGN 80
Qy 61 IGTGLLGLPLAVKNAGIVMGPISELLIIGIVAVHGMGILVKCAHHFCRRLNKSFVDYDGV 120
Db 81 IGTGLLGLPLAVKNAGIVMGPISELLIIGIVAVHGMGILVKCAHHFCRRLNKSFVDYDGV 140
Qy 121 MYGLESSPCSWLRNHAHWGRVVDFFLIYVTLQGCVCYFVFLADNFKQVIEAANGTTNCC 180
Db 141 MYGLESSPCSWLRNHAHWGRVVDFFLIYVTLQGCVCYFVFLADNFKQVIEAANGTTNCC 200
Qy 181 HNNETVILPTMDSRLYMLSFLPLVLLVFIKRLALSIFSLLANITMLVSLVMYQFIV 240
Db 201 HNNETVILPTMDSRLYMLSFLPLVLLVFIKRLALSIFSLLANITMLVSLVMYQFIV 260
Qy 241 -----QRIPDPDLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPKPFLLIL 292
Db 261 FRYMLSVFQRIIDPDLPLVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPKPFLLIL 320
Qy 293 YLGMVIVTILYISLGLGVLORGANIQSITLNLPCNLVQSVKLLYSIGIGFFTYALQFY 352
Db 321 YLGMVIVTILYISLGLGVLORGANIQSITLNLPCNLVQSVKLLYSIGIGFFTYALQFY 377
Qy 353 VPAEIIPFVSRAPHELCVVDLFRVTVLCLTILAILIPRLDLVLSVSVSSALA 412
Db 378 VPAEIIPFVSRAPHELCVVDLFRVTVLCLTILAILIPRLDLVLSVSVSSALA 436
Qy 413 LIIPPLEVTTFFYSEGMSPLTFKDALISILGFGVGVGTVEALYELIQSNAPIFINST 472
Db 437 LIIPPLEVTTFFYSEGMSPLTFKDALISILGFGVGVGTVEALYELIQSNAPIFINST 496
Qy 473 CAFI 476
Db 497 CAFI 500

RESULT 7

US-09-805-456-7
; Sequence 7, Application US/09805456
; Publication No. US20030170778A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001062
; CURRENT APPLICATION NUMBER: US/09/805,456
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 7
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human
US-09-805-456-7

Query Match      94.1%; Score 2324; DB 3; Length 476;
Best Local Similarity 94.5%; Pred. No. 3.3e-204;
Matches 450; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MSTQRLNEDYHDYSSSTDVSPSESEGLNNLSSPGSYQRFQGSNSTTWFQTLIHLKGN 60
Db 1 MSTQRLNEDYHDYSSSTDVSPSESEGLNNLSSPGSYQRFQGSNSTTWFQTLIHLKGN 60

Qy 61 IGTGLLGLPLAVKNAAGIVMGPIISLLIIGIVAVHCHMGILVKCAHFCRRLNKSFVDYGDV 120
Db 61 IGTGLLGLPLAVKNAAGIVMGPIISLLIIGIVAVHCHMGILVKCAHFCRRLNKSFVDYGDV 120

Qy 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180

Qy 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180

Qy 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240

Qy 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240

Qy 241 QRIIDPSHLPLVAPWKTYPLFFGTAFSFEIGVGLVPLENKMKOPRKPFLILYLGMVIT 300
Db 241 QRIIDPSHLPLVAPWKTYPLFFGTAFSFEIGVGLVPLENKMKOPRKPFLILYLGMVIT 300

Qy 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFTYALQFVVPAAIIP 360
Db 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFTYALQFVVPAAIIP 360

Qy 361 FVSRAPBHCBLVDLFRVTVLVCITCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420
Db 361 FVSRAPBHCBLVDLFRVTVLVCITCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420

Qy 361 VIVSWCKCCTLMVDLGGISAMLCCKTCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420
Db 361 VIVSWCKCCTLMVDLGGISAMLCCKTCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420

Qy 421 VTTFYSEGMSPLTIFKDALISILGFVGVGTVEALYELIOPSNAPIFINSTCAFI 476
Db 421 VTTFYSEGMSPLTIFKDALISILGFVGVGTVEALYELIOPSNAPIFINSTCAFI 476

RESULT 8
US-10-679-362-7
; Sequence 7, Application US/10679362
; Publication No. US20040146887A1
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO01062CON
; CURRENT APPLICATION NUMBER: US/10/679,362
; CURRENT FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Human
US-10-679-362-7

Query Match      94.1%; Score 2324; DB 4; Length 476;
Best Local Similarity 94.5%; Pred. No. 3.3e-204;
Matches 450; Conservative 9; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MSTQRLNEDYHDYSSSTDVSPSESEGLNNLSSPGSYQRFQGSNSTTWFQTLIHLKGN 60
Db 1 MSTQRLNEDYHDYSSSTDVSPSESEGLNNLSSPGSYQRFQGSNSTTWFQTLIHLKGN 60

Qy 61 IGTGLLGLPLAVKNAAGIVMGPIISLLIIGIVAVHCHMGILVKCAHFCRRLNKSFVDYGDV 120
Db 61 IGTGLLGLPLAVKNAAGIVMGPIISLLIIGIVAVHCHMGILVKCAHFCRRLNKSFVDYGDV 120

Qy 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180

Qy 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180
Db 121 MYGLESPCSMLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVIEAANGTTNNC 180

Qy 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240

Qy 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240
Db 181 HNETVILTPMDSRLYMLSFPLVLLVLFVTRNLRLALSIFSLLANITMLVSLVMIYQFIV 240

Qy 241 QRIIDPSHLPLVAPWKTYPLFFGTAFSFEIGVGLVPLENKMKOPRKPFLILYLGMVIT 300
Db 241 QRIIDPSHLPLVAPWKTYPLFFGTAFSFEIGVGLVPLENKMKOPRKPFLILYLGMVIT 300

Qy 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFTYALQFVVPAAIIP 360
Db 301 ILYISLGLCYLQFGANIQGSITLNLPCNLWYQSVKLLYSIGIFTYALQFVVPAAIIP 360

Qy 361 FVSRAPBHCBLVDLFRVTVLVCITCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420
Db 361 FVSRAPBHCBLVDLFRVTVLVCITCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420

Qy 361 VIVSWCKCCTLMVDLGGISAMLCCKTCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420
Db 361 VIVSWCKCCTLMVDLGGISAMLCCKTCLAILIPRLDLVISLVGSSVSSALALIIPPLLE 420

Qy 421 VTTFYSEGMSPLTIFKDALISILGFVGVGTVEALYELIOPSNAPIFINSTCAFI 476
Db 421 VTTFYSEGMSPLTIFKDALISILGFVGVGTVEALYELIOPSNAPIFINSTCAFI 476

Query Match      89.8%; Score 2217; DB 4; Length 434;
Best Local Similarity 90.8%; Pred. No. 1.9e-194;
Matches 432; Conservative 1; Mismatches 1; Indels 42; Gaps 1;

Qy 1 MSTQRLNEDYHDYSSSTDVSPSESEGLNNLSSPGSYQRFQGSNSTTWFQTLIHLKGN 60
Db 1 MSTQRLNEDYHDYSSSTDVSPSESEGLNNLSSPGSYQRFQGSNSTTWFQTLIHLKGN 60
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Db 300 VLYISLGLVQLQFADIKGSITLNLPCWLYQSVKLLYSIGIFFFTYALQFYVAEEIIP 359
Qy 361 FFVSRAPHELCVVDLFRVTVLVCITLAILPRDLVLSLGVSSSSALALIIPPLE 420
Db 360 AIVSRVPEFELVVDLSARTAMVCTCVLAVLPRDLVLSLGVSSSSALALIIPPLE 419
Qy 421 VTFYSGMSPLTIFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTAFI 476
Db 420 VTTYGGISPLTTTKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTAFI 475

RESULT 13
US-10-225-810-18
; Sequence 18, Application US/10225810
; Publication No. US20030157512A1
; GENERAL INFORMATION:
; APPLICANT: Berwingham, Jr., John R.
; TITLE OF INVENTION: Tramdorins and Methods of Using Tramdorin
; FILE REFERENCE: McLaugh-07165
; CURRENT APPLICATION NUMBER: US/10/225,810
; CURRENT FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-225-810-18

Query Match 86.6%; Score 2137.5; DB 4; Length 475;
Best Local Similarity 85.9%; Pred. No. 4.2e-187;
Matches 409; Conservative 32; Mismatches 34; Indels 1; Gaps 1;
Qy 1 MSTORLNEDYHDSSTDVSPSESPSGNLNLSPPGVSQRFQGSNTWFTQTLHLKGN 60
Db 1 MSTORLNEDYHDSSTDVSPSESPSGNLGSP-SPGYSYQLRGSSNTWFTQTLHLKGN 59
Qy 61 IGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHCHMGILVKCAHHFCRRLNKSPVDYDVT 120
Db 60 IGTGLGLPLAVKNAGLGLPLSLVIGIVAVHCHMGILVKCAHHLCRRLNKPFLDYDVT 119
Qy 121 MYGLESPCSWLRNHAHWRVDFLLIVTQLGFCVYFVLADNFKQVIEAANGTTTNC 180
Db 120 MYGLESPSTWVRNHSWGRRIIVDFLLIVTQLGFCVYFVLADNFKQVIEAANGTTTNC 179
Qy 181 HNNEVTILPTMDSRLYMSPFLPLVLTFRNLRLALSIFSLLANITMLVSLVMIYQFIV 240
Db 180 NNNVTIPTMDSRLYMSPFLPLVLTFRNLRLALSIFSLLANISMFVSLMIYQFIV 239
Qy 241 QRIPDPSHLPVAPWKTYPLFFGTAFISFEGIGMVLPLENKMKDPRKPFLLIYLGWVIT 300
Db 240 QRIPDPSHLPVAPWKTYPLFFGTAFIFAFEGIGVVLPLENKMKDSQKPFLLIYLGMAIT 299
Qy 301 ILYISLGLVQLQFADIKGSITLNLPCWLYQSVKLLYSIGIFFFTYALQFYVAEEIIP 360
Db 300 VLYISLGLVQLQFADIKGSITLNLPCWLYQSVKLLYSIGIFFFTYALQFYVAEEIIP 359
Qy 361 FFVSRAPHELCVVDLFRVTVLVCITLAILPRDLVLSLGVSSSSALALIIPPLE 420
Db 360 AIVSRVPEFELVVDLCVRWAMVCTCVLAILPRDLVLSLGVSSSSALALIIPPLE 419
Qy 421 VTFYSGMSPLTIFKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTAFI 476
Db 420 VTTYGGISPLTTTKDALISILGFVGVVGTVEALYELIQPSNAPIFINSTAFI 475

RESULT 14
US-10-291-737-4
; Sequence 4, Application US/10291737
; Publication No. US20030087299A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001017-CON
; CURRENT APPLICATION NUMBER: US/10/291,737
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/822,859
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/254,588
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Human
US-10-291-737-4

Query Match 77.5%; Score 1914; DB 4; Length 422;
Best Local Similarity 86.0%; Pred. No. 1.1e-166;
Matches 363; Conservative 33; Mismatches 26; Indels 0; Gaps 0;
Qy 51 QTLIHLKGNIGTGLGLPLAVKNAGIVMGPIISLLIIGIVAVHCHMGILVKCAHHFCRRLN 110
Db 1 QTLIHLKGNIGTGLGLPLAVKNAGLGLPLSLVIGIVAVHCHMGILVKCAHHLCRRLN 60
Qy 111 KSPVDYDVTVMYGLSPCSWLRNHAHWRVDFLLIVTQLGFCVYFVLADNFKQVI 170
Db 61 KPFLDYDVTVMYGLSPSTWIRNHSWGRRIIVDFLLIVTQLGFCVYFVLADNFKQVI 120
Qy 171 EAANGTTNCHNNETVILPTMDSRLYMSPFLPLVLTFRNLRLALSIFSLLANITMLV 230
Db 121 EAANGTTNCHNNETVILPTMDSRLYMSPFLPLVLTFRNLRLALSIFSLLANISMFV 180
Qy 231 SLVMIYQFIVQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRI 290
Db 181 SLVMIYQFIVQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRIQRI 240
Qy 291 ILYGMVITVILYISLGLVQLQFADIKGSITLNLPCWLYQSVKLLYSIGIFFFTYALQ 350
Db 241 ILYGMVITVILYISLGLVQLQFADIKGSITLNLPCWLYQSVKLLYSIGIFFFTYALQ 300
Qy 351 FYVPAEIIIPFFVSRAPHELCVVDLFRVTVLVCITLAILPRDLVLSLGVSSSSA 410
Db 301 FYVPAEIIIPVSRVPEFELVVDLSARTAMVCTCVLAVLPRDLVLSLGVSSSSA 360
Qy 411 LALIIPPLEVITTFYSGMSPLTIFKDALISILGFVGVVGTVEALYELIQPSNAPIFIN 470
Db 361 LALIIPPLEVITTFYSGMSPLTITKDALISILGFVGVVGTVEALYELIQPSNAPIFIN 420
Qy 471 ST 472
Db 421 ST 422

RESULT 15
US-10-365-564-4
; Sequence 4, Application US/10365564
; Publication No. US20030143623A1
; GENERAL INFORMATION:
; APPLICANT: WEBSTER, Marion et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001017-CIPCON
; CURRENT APPLICATION NUMBER: US/10/365,564
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US 09/822,859
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 60/254,588
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

; LENGTH: 422
; TYPE: PRT
; ORGANISM: Human
US-10-365-564-4

Query Match 77.5%; Score 1914; DB 4; Length 422;
Best Local Similarity 86.0%; Pred. No. 1.1e-166;
Matches 363; Conservative 33; Mismatches 26; Indels 0; Gaps 0;

Qy	51	QTLHLKGNIGTGLGPLAVKAGIYVKGPIISLLIIGIVAVHCHGIIIVKCAHFCRRLN	110
Db	1	QTLHLKGNIGTGLGPLAVKAGLGLGSLVIGIVAVHCHGIIIVKCAHLCRRLN	60
Qy	111	KSFVDYGDVVMYGLESSPCSWLRNHAHWGRVDFFLIVTQLGFCVYFVFLADNFKQVI	170
Db	61	KPFLDYGDVVMYGLCSFSTWIRNHSWGRRIIVDFLVVTLQGFCCVYFVFLADNFKQVI	120
Qy	171	BAANGTTNCHNNETVILTPMDSRLYMLSPFLVLLVFIIRNLRAISFILLANITMLV	230
Db	121	BAANGTTNCHNNETVILTPMDSRLYMLTFLPFLVLLSFIRNLRILSFILLANISMFV	180
Qy	231	SLVMYQFIVORIPDPSHLPLVAPWKTYPLFEGTAFISFEGIGMVLPLENKMOKPKPPL	290
Db	181	SLMIYQFIVORIPDPSHLPLVAPWKTYPLFFGTAFIFEGIGVVLPLENKMOKSQKPPL	240
Qy	291	ILYLGMIIVTIIYISLGLGYLQFGANIQGSITLNLPCWLYQSVKLLYSIGIFFYALQ	350
Db	241	ILYLGMAIIVTIIYISLGLGYLQFGADIKGSITLNLPCWLYQSVKLLYSIGIFFYALQ	300
Qy	351	FYPVABIIIPFVSRAPEHCELVLDLTVRTVLVCLTILAILPRLDLIVISLVGSVSSA	410
Db	301	FYVAAEIIIPAVSRVPERFELVDLSARTAMVCVLCVAVLIPRLDLIVISLVGSVSSA	360
Qy	411	LALIIPPLLEVTFYSECMSPITIFKDALISILGFGVGVCTYEALYELIOPSNAPIETN	470
Db	361	LALIIPPLKLVTTYEGISPLTITKDALISILGFGVGVGVGYESLWELIOPSHSDSTN	420
Qy	471	ST	472
Db	421	ST	422

Search completed: August 24, 2006, 01:29:45
Job time : 186 secs

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OM protein - protein search, using sw model

Run on: August 24, 2006, 01:26:49 ; Search time 33 Seconds
(without alignments)
977.303 Million cell updates/sec

Title: US-10-679-362-2
Perfect score: 2469
Sequence: 1 MSTQLRNEDYHDSYTDVS.....YELIQSNAPIFINSTCAFI 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 243793 seqs, 67754213 residues

Total number of hits satisfying chosen parameters: 243793

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1255.5	50.9	504	6	US-10-505-928-42
2	972.5	39.4	369	7	US-11-293-697-3609
3	465.5	18.9	436	6	US-10-953-349-368
4	410.5	16.6	371	6	US-10-953-349-369
5	405	16.4	425	6	US-10-449-902-37011
6	405	16.4	425	6	US-10-449-902-49196
7	404.5	16.4	422	6	US-10-449-902-32842
8	404.5	16.4	422	6	US-10-449-902-53550
9	402.5	16.3	422	6	US-10-449-902-53486
10	400	16.2	395	6	US-10-449-902-29254
11	382	15.5	355	6	US-10-953-349-370
12	339.5	13.8	342	6	US-10-449-902-32686
13	332	13.4	349	6	US-10-449-902-36917
14	318	12.9	531	7	US-11-174-307B-5170
15	302	12.2	468	7	US-11-056-355B-105677
16	302	12.2	468	7	US-11-056-355B-116916
17	302	12.2	474	7	US-11-056-355B-105676
18	302	12.2	474	7	US-11-056-355B-116915
19	302	12.2	550	7	US-11-056-355B-105675
20	302	12.2	550	7	US-11-056-355B-116914
21	300.5	12.2	436	7	US-11-056-355B-54601
22	300.5	12.2	448	7	US-11-056-355B-54600
23	300.5	12.2	458	7	US-11-056-355B-54599
24	292	11.8	471	7	US-11-056-355B-79663
25	292	11.8	526	7	US-11-056-355B-79662

26	291.5	11.8	453	7	US-11-056-355B-75679	Sequence 75679, A
27	291.5	11.8	470	7	US-11-056-355B-75678	Sequence 75678, A
28	291.5	11.8	537	7	US-11-056-355B-75677	Sequence 75677, A
29	281	11.4	410	7	US-11-056-355B-96651	Sequence 96651, A
30	281	11.4	469	7	US-11-056-355B-96650	Sequence 96650, A
31	281	11.4	550	7	US-11-056-355B-96649	Sequence 96649, A
32	276	11.2	536	7	US-11-056-355B-36517	Sequence 36517, A
33	276	11.2	536	7	US-11-056-355B-44879	Sequence 44879, A
34	266.5	10.8	558	6	US-10-953-349-8582	Sequence 8582, Ap
35	266.5	10.8	558	6	US-10-953-349-8582	Sequence 8582, Ap
36	266.5	10.8	559	6	US-10-953-349-34887	Sequence 34887, A
37	266.5	10.8	559	7	US-11-056-355B-8581	Sequence 8581, Ap
38	266.5	10.8	574	6	US-10-953-349-34886	Sequence 34886, A
39	266.5	10.8	574	7	US-11-056-355B-8580	Sequence 8580, Ap
40	264	10.7	377	7	US-11-056-355B-36518	Sequence 36518, A
41	264	10.7	377	7	US-11-056-355B-44880	Sequence 44880, A
42	261.5	10.6	258	6	US-10-449-902-42650	Sequence 42650, A
43	261	10.6	413	6	US-10-449-902-38581	Sequence 38581, A
44	260.5	10.6	571	6	US-10-449-902-52309	Sequence 52309, A
45	258	10.4	371	7	US-11-056-355B-79664	Sequence 79664, A

ALIGNMENTS

RESULT 1

US-10-505-928-42
; Sequence 42, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 42
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-505-928-42

Query Match	50.9%	Score 1255.5;	DB 6;	Length 504;
Best Local Similarity	52.0%	Pred. No. 5.4e-96;		
Matches	254;	Conservative	80;	Mismatches 119; Indels 35; Gaps 6;
Qy	6	LRNEDYHDSYSDVSPSPSEGLNNLSFGSYQRFQGSNSTTWFQTLIHLKKNIGTGL	65	
Db	26	LINEQNFDTGSDERHEQE-----LLPVQKHVQLDDQEGISFVQTLMLHLKKNIGTGL	77	
Qy	66	LGLPLAVNAGIVGMPISLLIIGIVAHVCMGILVKCAHFCRRLNKSFVDYGDVTWYCLE	125	
Db	78	LGLPLAKNAGIVLGPISLVFIGIISVHCMIHLCVRCSHFLCLRFKFKSLGYSVDTVSFAME	137	
Qy	126	SSPSCWLRNHAHGRVVDVFLVITQLGFCVCYVFELADNFKOV-----IEAANG	175	
Db	138	VSPWSCLOKQAAWGRSVVDVFLVITQLGFCVYVFLAENVKQVHGFLESKVFSNSTN	197	
Qy	176	TTNNCHNETVILPTTMDSLYMLSFPLFVLVILFIRNLRALSIFSLANITMLVSLYMI	235	
Db	198	SSNFCERR-----SVDLRIYMLCFPLFIALLVFIRELKNLFLVLSFLANYSMAVSLVII	250	
Qy	236	YQFTVQRIPDPSPHPLVAPWKTYPLFTGTALFSPSEGIGMVLPLENOMKDPKRPFLIYLGL	295	
Db	251	YQYVVRNMPDHPNLPVAGWKYPLFTGTAVFAFEGIGVLPLENQMKESKRFPQALNIG	310	
Qy	296	MVITVILYISLGCILGYLQFGNIOGSIITNLP-NCWLYQSVKLLYSIGIFFTYALQFVVP	354	
Db	311	MGIVTTLYVTLATLGYMCFHDEIKGSIITNLPQDVMWLYQSVKILYSFGIFVTSIQFVVP	370	

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QY 355 AEIIIPFVSRAPEHCELVVDLFRVTVLVCLTCILAILPRDLVLISLVGSSSSALALI 414
Db 371 AEIIIPGITSKFHTKWKQICEFGIRSELVSITCAGAILIPRLDIVISFVGAVSSSTIALI 430
QY 415 IPLLLEVTTFYSEGMSPLTIFKDALISILGFGVGVGTVEALYELIOPS-----NAP 466
Db 431 LPLLEVLTSKSHYNTWMLKNISIAFTGVGVGLLGTITVEEIIYTPKVVAGTPOSP 490
QY 467 IF-INSTC 473
Db 491 FLNLNSTC 498

RESULT 2
US-11-293-697-3609
; Sequence 3609, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cdNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3609
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3609

Query Match 39.4%; Score 972.5; DB 7; Length 369;
Best Local Similarity 53.0%; Pred. No. 9e-73;
Matches 196; Conservative 63; Mismatches 84; Indels 27; Gaps 5;

QY 124 LESSPCSWLRNHAHWRRVVDFFLIIVTQLGCCYVFFVLADNFKQV-----IEAA 173
Db 1 MEVSPWCSLQQAAGRSVVDFFLIVITQLGFCSVIIVFLAENKQVHEGFLESKVFISS 60
QY 174 NGTNNCHNETVILTMTDSRLYMLSFPLVLVIRNLRLSIFSLANITMLVSLV 233
Db 61 TNSNPNCCRR-----SVDLRIYMLCLFPFIILLVFIRELKNLFLVLSFLANVSMVSLV 113
QY 234 MIYQIFVQRIIDPSHLPVAPWKTYPLFFGTAIFSFEIGMVLPLENKMKDPRKFPILY 293
Db 114 IYQYVVRNPDPPHNLPIVAGKKYPLFFGTAVPAFEGIGVVLPLENQMKESRFPQALN 173
QY 294 LGMVIVTILYISLCLGYLQFGANIQSITLNLPL-NCWLYQSVKLLYSIGIFFTYALQFY 352
Db 174 IGMGIIVTLVTLATGVMCFRDEIKGSITLNLDPQDVWLYQSVKILYSFGIFVYSIQFY 233
QY 353 VPABIIIPFVSRAPEHCELVVDLFRVTVLVCLTCILAILPRDLVLISLVGSSSSALA 412
Db 234 VPABIIIPGITSKFTKWKQICEFGIRSFVLSITCAGAILIPRLDIVISFVGAVSSSTLA 293
QY 413 LIIPPLEVTTFYSEGMSPLTIFKDALISILGFGVGVGTVEALYELIOPS-----N 464
Db 294 LILPPLVEILTFSEKHYNWMLKNISIAFTGVGVGLLGTITVEEIIYTPKVVAGTPO 353
QY 465 APIF-INSTC 473
Db 354 SPFLNLNSTC 363

RESULT 3
US-10-953-349-368
; Sequence 368, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: US/10/953,349
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 369
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-368

Query Match 16.6%; Score 410.5; DB 6; Length 371;
Best Local Similarity 32.0%; Pred. No. 2.4e-26;
Matches 132; Conservative 60; Mismatches 143; Indels 77; Gaps 14;

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 368
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-368

Query Match 18.9%; Score 465.5; DB 6; Length 436;
Best Local Similarity 32.4%; Pred. No. 8.2e-31;
Matches 143; Conservative 66; Mismatches 155; Indels 77; Gaps 14;

QY 50 FOTLIHLKGNIGTGLGLPLAVKNAGIVMGPTSLTIIGIVAVHCMGILVKCAHHCRRRL 109
Db 37 FKTFAVNFIAVAGAGVGLPYAFKRTGWLGMVLLVSVSLVTHCMMLLV-----YTRRK 91
QY 110 NKSP-----VDYGDVTVMYGLESPSCSWLRNHAHWRRVVDFFLIIVTQLGCCYVFFVL 162
Db 92 LDSFNAGISKIGSFGD-----LGFVCGSL-----GRIVVDLFIILSQAGFCVGLIFI 140
QY 163 ADNFQVIEAANGTT--NNCHNETVILTPT-----MDSLYMLSELPL 205
Db 141 -----GTTLANLSDPE-----SPTSLRHQTRLGSEFLGVSSKSLYIWGCFPFQ 184
QY 206 VLLVFRNLRLSIFSLANI-----TMLVSLVMYQIFVQRIIDPSHLPVAPWKTYPLF 261
Db 185 LGLNSIKTHTLAPLSIFADIVDLGAMAVVIVEDSMILKQRPD-----VVAFGMSLF 238
QY 262 ---FGTAIFSFEIGMVLPLENKMKDPRKFPPLIYLGWIVITLYISLCLGYLQFGANI 318
Db 239 LYGMGVAVYSFEGVMVLPLESEMCKDKFGKVLALGMGFIISLYIAFGILGYLAFGEDT 298
QY 319 QGSITLNLPCWLYQSVKLLYSIGIFFTYALQFYVPAEIIIPFVSRAPEHCELVVDL 378
Db 299 MDIITANLGAGLVSTVQLGLCNLFFTPPLMNNPVFEIVERRP-SRG-----MYSAWL 351
QY 379 RTVLVCLTCLAILPRDLVLISLVGSSSSALALIIPPLEVTTFYSEGMSPLTIFKDA 438
Db 352 RWVLVLAIVLVALFVFNADFLSLVSSCCCVLGFVLPAFLHLLVF-KEEMGWLQWSSDT 410
QY 439 LISILGFGVGVGTVEALYEL 459
Db 411 AIVVLGWLAVSGTWSSLSSEI 431

RESULT 4
US-10-953-349-369
; Sequence 369, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 369
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-369

Query Match 16.6%; Score 410.5; DB 6; Length 371;
Best Local Similarity 32.0%; Pred. No. 2.4e-26;
Matches 132; Conservative 60; Mismatches 143; Indels 77; Gaps 14;

QY 79 MGPIISLLIIGIVAVHCMGILVKCAHHCRRRLNKSF-----VDYGDVTVMYGLESPSCSW 131
```

```
Db 1 MGVLVSVSVLTHHMLLV-----YTRRKLDSEFNAGISKIGSEGD-----LGFVAVCGS 50
Qy 132 LRNHAHMRVVDVDFLIYVQLGFCVYFVFLADNFKQVIEAANGTT--NNCHNNETVILTP 190
Db 51 L-----GRIVVDLFIILSQAGFCVGLIFI-----GTTLANLSDPE-----SP 88
Qy 191 T-----MDSLYMLSFLLPFLVLLVFLRNLRALSIFSLANI-----TMLV 230
Db 89 TSLRHQFTRLGSEFLGVSSKSLYIYWGCFPLQGLNSIKTLTHLAPLSIFADIVDLGAMAV 148
Qy 231 SLVMIYQIVQRIIPDPHPLVAPKTYPLF---FGTAIFSEFGIGMVLPLENKKDKPRK 287
Db 149 VIVEDSMILKORPD-----VWAPFGMSFLYGMGVAVYFEGVGMVLPLESEMKDKD 202
Qy 288 PFLILYLGWIVTILYISGLGCLYQFGANIQSGITLNLNPNCWLYSQSVKLLYSIGIFTY 347
Db 203 FGKVALGGMGFSIYIYAFILGILYAFEGEDTMDITANLGLAGLYSTVVQLGCLINLFTTF 262
Qy 348 ALQFYVPAEIIIPFVSRAPHELCVLDLVRTVVLVCLTCLAILIPRLDLVLSLVGSVS 407
Db 263 PLMNPVEIIVERRF-SRG-----MYSAMLRWVLVLAVALVFPNFAFDPLSLVGSST 315
Qy 408 SSALALIIPPLEVTTFFYSEGMSPLTIKDALISILGFVGVGTYEALYEL 459
Db 316 CCVLGFLPALFHLVLF-KEEMGLQWSSDTAIVVLGVVLAVSGTWSSLSBI 366
```

RESULT 5

```
US-10-449-902-37011
; Sequence 37011, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 37011
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-37011
```

```
Query Match 16.4%; Score 405; DB 6; Length 425;
Best Local Similarity 27.6%; Pred. No. 8e-26;
Matches 120; Conservative 81; Mismatches 164; Indels 70; Gaps 13;

Qy 51 QTLHLKGNITGTLGLPLAVKNGIWMGSPISILLIIGIVAVHCGMILVKAHFCRRL- 109
Db 39 KTFANVFIAVVGSGVLGPLYTFSRTGWAGSVLLLAVALTFHCHMLLVACR----RRLA 94
Qy 110 --NKSFDYDGTVMYGLSSPCSLRNHAGRRVVDFFLIYVQLGFCVYFVFLADNFK 167
Db 95 YDHPKIASFGD-----LGAAVC-----GPAGRHVVDAMLVLSQASFCVGLIFISNTMA 143
Qy 168 QVIEAANGTTNNCHNNETVILTPMDSR-LYMLSFLPFLVLLVFIIRNLRALSIFSLANI 226
Db 144 HLYPVGDSPPS-----SPLLTAKAIFIWMLPFQGLNSIKTLTLLAPLSIFADV 193
Qy 227 TMLVSL-VMYQIVQRIIPDPHPLVAPW--KTYPLF-----FGTAIFSEFGI 272
Db 194 VDLGAMGVVLGDQ-----VSTWLANKPPVPFASAGPTILYGLGVAVYAFEGI 240
Qy 273 GMVLPLENKKMDPRKFPILLYLGWIVTILYISGLGCLYQFGANIQSGITLNLNPNCWLY 332
Db 241 GMVLPLEAERADKRFKGGTTLALSMFAIVMVLFGAMGYLAFGAATRIIITNLGTGMLS 300
Qy 333 QSVKLLYSIGIFTYALQF---YVPAEIIIPFVSRAPHELCVLDLVRTVVLVCLTCL 389
Db 301 VTQVLGCLINLFFTPMVMNPVYEAERLL-----CRKYAWMLRWLLVMVVGML 350
Qy 390 AILPRLDLVLSLVGSSVSSSALALIIPPLEVTTFFYSEGMSPLTIKDALISILGFVGV 449
Db 351 AMLVPNFADFLSLVGSSVCLLGFVLPAAFLHKVFGAEVGP-GLAGDVAIVVVGTLAV 409
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Qy 273 GMVLPLENKKMDPRKFPILLYLGWIVTILYISGLGCLYQFGANIQSGITLNLNPNCWLY 332
Db 241 GMVLPLEAERADKRFKGGTTLALSMFAIVMVLFGAMGYLAFGAATRIIITNLGTGMLS 300
Qy 333 QSVKLLYSIGIFTYALQF---YVPAEIIIPFVSRAPHELCVLDLVRTVVLVCLTCL 389
Db 301 VTQVLGCLINLFFTPMVMNPVYEAERLL-----CRKYAWMLRWLLVMVVGML 350
Qy 390 AILPRLDLVLSLVGSSVSSSALALIIPPLEVTTFFYSEGMSPLTIKDALISILGFVGV 449
Db 351 AMLVPNFADFLSLVGSSVCLLGFVLPAAFLHKVFGAEVGP-GLAGDVAIVVVGTLAV 409
Qy 450 VGTYEALYELIOPSN 464
Db 410 SGTWTSLAQIFSSD 424
```

RESULT 6

```
US-10-449-902-49196
; Sequence 49196, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 49196
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-49196
```

```
Query Match 16.4%; Score 405; DB 6; Length 425;
Best Local Similarity 27.6%; Pred. No. 8e-26;
Matches 120; Conservative 81; Mismatches 164; Indels 70; Gaps 13;

Qy 51 QTLHLKGNITGTLGLPLAVKNGIWMGSPISILLIIGIVAVHCGMILVKAHFCRRL- 109
Db 39 KTFANVFIAVVGSGVLGPLYTFSRTGWAGSVLLLAVALTFHCHMLLVACR----RRLA 94
Qy 110 --NKSFDYDGTVMYGLSSPCSLRNHAGRRVVDFFLIYVQLGFCVYFVFLADNFK 167
Db 95 YDHPKIASFGD-----LGAAVC-----GPAGRHVVDAMLVLSQASFCVGLIFISNTMA 143
Qy 168 QVIEAANGTTNNCHNNETVILTPMDSR-LYMLSFLPFLVLLVFIIRNLRALSIFSLANI 226
Db 144 HLYPVGDSPPS-----SPLLTAKAIFIWMLPFQGLNSIKTLTLLAPLSIFADV 193
Qy 227 TMLVSL-VMYQIVQRIIPDPHPLVAPW--KTYPLF-----FGTAIFSEFGI 272
Db 194 VDLGAMGVVLGDQ-----VSTWLANKPPVPFASAGPTILYGLGVAVYAFEGI 240
Qy 273 GMVLPLENKKMDPRKFPILLYLGWIVTILYISGLGCLYQFGANIQSGITLNLNPNCWLY 332
Db 241 GMVLPLEAERADKRFKGGTTLALSMFAIVMVLFGAMGYLAFGAATRIIITNLGTGMLS 300
Qy 333 QSVKLLYSIGIFTYALQF---YVPAEIIIPFVSRAPHELCVLDLVRTVVLVCLTCL 389
Db 301 VTQVLGCLINLFFTPMVMNPVYEAERLL-----CRKYAWMLRWLLVMVVGML 350
Qy 390 AILPRLDLVLSLVGSSVSSSALALIIPPLEVTTFFYSEGMSPLTIKDALISILGFVGV 449
Db 351 AMLVPNFADFLSLVGSSVCLLGFVLPAAFLHKVFGAEVGP-GLAGDVAIVVVGTLAV 409
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	Query Match	15.5%	Score 382;	DB 6;	Length 355;
	Best Local Similarity	32.8%	Pred. No. 5.1e-24;		
	Matches 122; Conservative	51;	Mismatches 131;	Indels 68;	Gaps 12;
Qy	112 SFVDYDGTVMYGLSSPCSWLRNHAHWGRVDFFLIVTGLGFCVVVFELADNFKQVIE	171			
Db	23 SFGDLGFAV-----CGSL-----GRIVDLFIILSQAGFCVGYLIFI-----	59			
Qy	172 AANGTT--NNCHNETVILTPT-----MDSRLNMLSPFLPVLVLVFTRLNL	214			
Db	60 ---GTTLANLSDPE---SPTSLRHQFTRLGSEBFLGVSSKSLAIWGCFFPQLGINSIKTL	112			
Qy	215 RALSISFLIANI---TMLVSLVMYQFIVQRIIPDPSHLPVAPWKTYPLF---FGTAIF	267			
Db	113 THLAPISIFADIVDLGMAVIVEDSMIIILKQRP-----VVAFGMSLFLYGMGVAVY	166			
Qy	268 SFEGIGMVLPLENMKDPKRPFLIYLGLMVIVITLYISLCLGYLQFAGNIQGSITUNLP	327			
Db	167 SFGVGWVILPESMKDKDFEGKVLALGMGFISLYIAFGILGYLAFEGEDMTDIITANLG	226			

```
QY 328 NCWLYOSVKLLYSIGIFFTYALQFYVPAEIIIPFFVSRAPEHCHELVVDLFFVTRTVLVLCTC 387
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 227 AGLVSTVQLGCLNLFPTFLMNPVFEIVERRF-SRG-----MYSAMLRWVLAVT 279
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 388 ILAILPRDLVLSVGSVSSALALIIPLEVTTFYSEGMSPLTFKDALISILGFVG 447
      :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 280 LVALFVFNADFLSLVSGSCCVLGFVLPALFHLVF-KEEMGLOWSSDTAIVLGLVWL 338
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 448 FVVGTYEALVEL 459
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 339 AVSGTWSSLSSEI 350
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 12
US-10-449-902-32686
; Sequence 32686, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32686
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-32686

Query Match 13.8%; Score 339.5; DB 6; Length 342;
Best Local Similarity 27.5%; Pred. No. 1.6e-20;
Matches 107; Conservative 67; Mismatches 150; Indels 65; Gaps 12;

QY 95 MGLIVKCAHHFCRRLNK--SFVDYGDVTMYGLESSPCSWLRNHAHMGRRVVDFFLIVTQL 152
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MMLLVACRRRLADEHPKIASFGDLGDAVFRG-----P-----CRLAVDTMLVLSQA 46
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 153 GFCCVYFVFLADNPKQVIEANGTNNCHNETVILPTWDSRLYMLSFPLVLLVFI 212
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 47 SFCVGYLIFISNTMAHLYPVFAPSSN-----ALLSP---KALFIWAMLPFQGLNSIK 96
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 213 NLRALSIFSLANITMLVSLVMYQFIVQRIQIPDPSHLPLVAPW--KTYPLF----- 261
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 97 TLTLAPLSIFADVVDLGAMGVILG-----EDVSVLAKPPVPFAGGLSAIL 144
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 262 --FGTAFSPFEGIGWLPLENKMDPKRPFLLILYLGWIVITLYISICGLYQFGANIQ 319
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 YGIGVSUYAFEGIGWLPLEBAANKKFGTGLSGMGTAVMYGLFGAMGYAFADTR 204
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 320 GSITLNPNCWLYOSVKLLYSIGIFFTYALQF---YVPAEIIIPFFVSRAPEHCHELVVDL 376
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 DIITNLGTGWLSSAAVQLGCLNLFFTMPVMHPVYEVRLL-----HGKRYC-----W 254
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 377 FVRVIVLCLTILAILPRDLVLSVGSVSSALALIIPLEVTTFYSEGMSPLTFK 436
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 255 WLRWLLVAVGLSAMYVNFDFIALVSGSSVCVVLGFLVPASFLKVFGEAE-MWSGVLS 313
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 437 DALISILGFVGFFVVGTYEALVELIQPSNA 465
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 314 DVLLVLLGLSLAVGTGTYTSLAQIHFSSSA 342
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
```

```
US-10-449-902-36917
; Sequence 36917, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36917
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Oryza sativa
; US-10-449-902-36917

Query Match 13.4%; Score 332; DB 6; Length 349;
Best Local Similarity 27.6%; Pred. No. 6.8e-20;
Matches 96; Conservative 61; Mismatches 145; Indels 46; Gaps 9;

QY 135 HAHM-----GRRVDFFLIVTQLGFCVVFVFLADNFKQVIEAANGTTNNCH 181
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 HGHTYVDGLGEKCFGTIGRCLTEILIVSQAGSVAYLIFIGNL-----H 66
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 NNETVILPTMDSRLYMLSFPLVLLVTRINLRALSIFSLANITMLVSLVMYQFIVQ 241
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 SVFSQLMSP---AAFIFAILLPQIALSFIRLSLSPFSIFADVCNVLAMAIKEDLQ 123
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 242 RIPDP--SHLPLVAPWKTYPLFFGTAFISFEGIGWLPLENKMDPKRPFLLILYLGWIV 299
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 LFDHPFANRSASFNLW-AIPFTFEGVAFCEPFGFSMTLALSSMAERKFRWVLSQAVVG 182
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 300 TILYISICGLYQFGANIQGSITLNPNCWLYOSVKLLYSIGIFFTYALQFVVPABII 359
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 IIVYACFVCGVLAAYGEATKDIIITLNPNSWSSAAVKVGLCIALVFTFPVMMHPHIVE 242
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 360 PFF-----VSRAPHECHELVVDLFFVTRTVLVLCTCILAILPRDLVLSVGSVSSAL 411
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 ERQSSGCFPKLSHKVYRGAEWVGLHSSRIVMVTILSVVASFIPAFGFSIFSVGSTVCALL 302
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 412 ALIIPLEVTTFYSEGMSPLTFKD--ALISILGFVGFFVVGTYEALY 457
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 SFVLPTIFHL-SIVGSSMSPRRWGDYGFLLFLGLGFAGY--GLIRALF 347
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
US-11-174-307B-5170
; Sequence 5170, Application US/11174307B
; Publication No. US20060143729A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai
; APPLICANT: BROVER, Vyacheslav
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY
; TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1601PUS2
; CURRENT APPLICATION NUMBER: US/11/174,307B
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: 60/583,671
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,781
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: 60/583,651
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 5544
; SEQ ID NO 5170
```

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; LENGTH: 531
; TYPE: Prt
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: Pfam Name: Aa_trans; Pfam Description: Transmembrane amino
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50904567; NR Description: putative amino acid
; OTHER INFORMATION: transport protein [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|41053220|dbj|BAD08181.1| putative amino acid transport protei
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 50915446; NR Description: amino acid
; OTHER INFORMATION: transporter-like [Oryza sativa (japonica cultivar-group)]
; OTHER INFORMATION: >gi|47497045|dbj|BAD13097.1| amino acid transporter-like [Oryza
; OTHER INFORMATION: sativa (japonica cultivar-group)] >gi|47497767|dbj|BAD19867.1|
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 30687791; NR Description: amino acid transporter
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 42563875; NR Description: amino acid transporter
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: GI Number: 42563873; NR Description: amino acid transporter
; OTHER INFORMATION: GI Number: 42563873; NR Description: amino acid transporter
US-11-174-307B-5170

Query Match      12.9%; Score 318; DB 7; Length 531;
Best Local Similarity 25.8%; Pred. No. 1.6e-18;
Matches 115; Conservative 73; Mismatches 175; Indels 82; Gaps 18;

Qy 42 GQSTNTWFOQLHLLKNGTIGLGLPLAVKNAGVMPISLLIIGIVAVHC--MGILV 99
Db 140 GQGSVT--QTFNGINVLAVGLLSAPFTIHEAGWA-----GLAVLSFALICCYTGVL 193
Qy 100 KCAHFHRRLNKSFVDYGDVTVMYGLESPCSWLRNHAHWR--RVDPFLIVTQLGFCV 157
Db 194 K----HCFESKDGATYDI-----GEAFGRIGRLIISILYELYSYCV 235
Qy 158 YFVFL-ADNFQVTEAANGTTNNCHNETVILPTMDSRLYMLSPFLPLVLL--VFIRNL 214
Db 236 EFIILEGDMNTSIFPDVNINLFGIH-----VDSK-HFFGVLTALVVLPTVWLRDL 284
Qy 215 RALSIFS--LLANITMLVSLVMI-----YQFIVQIPDPHPLVAPPKTYPLPFG 263
Db 285 RVLSYLSAGGVIAITLWFLSVALVGTTEGIFHQ-----TGBAVKWSGMPPAIG 333
Qy 264 TAIFSFEIGMVLPLENKQKDPKRPPLILYLGWIVITILYISLGLCYLOFGANIQGSIT 323
Db 334 IYGCYSGHVPPIYQMSDRTPFKALFICFAVCTAIYGSFALIGYLMFGDKTLSOIT 393
Qy 324 LNLPCMLYQSVKLLYS-IGIFFTVALQFYVPAEIIIPFFVSRAPHC-----ELVVD 375
Db 394 LNLKESPAKVALWTVTINPFTKAL-----LLNP--LARSLEELRPEGFLNETIVS 444
Qy 376 LFRVTVLCLTILAILPRDLVLISVSGSVSSALALIIPPLEVITFYSEGMSPLTIF 435
Db 445 IILRTSLVASTVIAFLPFFGLVNALIGSLLSILVAVIMPALCFKIAQNKAIRPQVIA 504
Qy 436 KDALISILGVGVGVVGYEALVELI 460
Db 505 SVAIL-VVGVISALGTYSVASII 528
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RESULT 15

US-11-056-355B-105677

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; Sequence 105677, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 105677
; LENGTH: 468
; TYPE: Prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(468)
; OTHER INFORMATION: Ceres Seq. ID no. 13617748
US-11-056-355B-105677

Query Match      12.2%; Score 302; DB 7; Length 468;
Best Local Similarity 25.3%; Pred. No. 2.9e-17;
Matches 123; Conservative 87; Mismatches 188; Indels 88; Gaps 20;

Qy 2 STQRLNEDYHDYST--DVSPESSPEGLNNLSSPGSYQRFQGSNSTTWFQTLIHLK 59
Db 37 SSRKLLSQPDPDKETILPVNPQSLKSLVTDLP-----EPNLCSFSQSVLNGTNV 89
Qy 60 NIGTGLGLPLAVKNAGVMPISLLIIGIVAVHGMILVKCAHFCRRLNKS-----FV 114
Db 90 LCGLGLITMPVAIKESGWLGLPI-LLPFGVITCY-TGVLMK-----RCLSSSPGIQYTP 141
Qy 115 DYGTVMYGLESPCSWLRNHAHWRVDFLIVTQLGFCVYFVFLADN----FKOV- 169
Db 142 DIGQAA-FGIT-----GRFIISILLVELYAAACVEYIIMSDNLSGLFPNVS 187
Qy 170 IEAANGTTNNCHNETVILPTMDSRLYMLSPFLPLVLLVFIIRNLALSIFS---LLANI 226
Db 188 LSIASGIS-----LDSQIFAILTTLVLP---TWLKDLSLLSYLSVGVGLASI 234
Qy 227 TMLVSLVMIYQ-----FIVQIPDPHPLVAPPKTYPLPFGTAIFSFEIGMVLPLEN 280
Db 235 LLGICLEWVGAVDGIQFATGRVFDLSNLPV-----IGIFGFGYSGHVSFPPNIYS 285
Qy 281 KMKDPRKPLILYLGWIVITILYISLGLCYLOFGANIQGSITLNLPCMLYQSVKLLYS 340
Db 286 SMKDPSPRLVLVTCFSCTVLYIAVAVCGYTMFEAVESQFTLNPMPKHFFPSKVAVMTA 345
Qy 341 IGIFFT-YAL--QFYVPAEIIIPFFVSRAPHCVELVVDLFRVTVLCLTILAILPRL 396
Db 346 VITPMTKALTITIVMSLEELIPTAKMRSG-----VSILFRMLVTLVTLVSVFF 400
Qy 397 DLVLSVSGSVSSALALIIPPLEVITF---YSEGMSPLTIFKDALISILGFVGVFVGT 453
Db 401 AIVAAALIGSFLAMLVALIFPCGLCYLSILKGLSNTQIGLCIF---IIVFGVSGCCGT 456
Qy 454 EALVEL 459
Db 457 SAISRL 462
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Job time : 34 secs

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